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(71) Applicants: **F. HOFFMANN-LA ROCHE AG**
[CH/CH]; 124 Grenzacherstrasse, CH-4070 Basel (CH).
SINOGENOMAX CO. LTD. CHINESE NATIONAL
HUMAN GENOMECENTER [CN/CN]; 3#-707 North
Yongchang Road BDA, 100176 Beijing, PR. (CN).

(72) Inventors: **CHEN, Jie**; Department of Pathology, Peking
Union Medical Coll, ege Hospital, Chinese Academy of
Medical Science, Peking Union Medical College, Beijing
100730 P.R. (CN). **HU, Liping**; National Laboratory of
Medical Molecular Biology, Institute of Basic Medical
Sciences, Chinese Academy of Medical Science + Peking
Union Medical Coll, ege, Beijing 100005, P.R. (CN).
LIU, Tong, Hua; Department of Pathology, Peking Union
Medical Coll, ege Hospital, Chinese Academy of Medical
Science, Peking Union Medical College, Beijing 100730,
P.R. (CN). **LU, Zhao, Hui**; Department of Pathology,

Peking Union Medical Coll, ege Hospital, Chinese Acad-
emy of Science, Peking U, nion Medical College, Beijing
100730, P.R. (CN). **SHEN, Yan**; c/o Chinese National
Human Genome Center, Beijing SinoGenoMax Co. Ltd.,
#3-707 North Yongchang Road BDA, Beijing 100176
(CN).

(74) Common Representative: **WITTE, Hubert**; 124 Gren-
zacherstrasse, CH-4070 Basel (CH).

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(54) Title: **SPECIFIC MARKERS FOR PANCREATIC CANCER**

(57) Abstract: The present invention provides polypeptides which are up- or down-regulated in pancreatic cancer and which can be used as markers for diagnosis of pancreatic cancer. The invention also provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological sample; and b) detecting and/or measuring the increase of one or more polypeptides as disclosed herein. Furthermore, screening methods relating to inhibitors and antagonists of the specific polypeptides disclosed herein are provided.

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Specific Markers for Pancreatic Cancer

The present invention relates to markers for diagnosis of pancreatic cancer comprising at least one polypeptide identified by proteomics to be up-regulated in pancreatic cancer, to an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological
5 sample; and b) detecting and/or measuring the increase of specific markers as disclosed herein. Furthermore, screening methods relating to antagonists of the specific markers disclosed herein are provided.

10 Pancreatic cancer is a common cause of death in the Western world. It is one of the most aggressive malignant tumors, with an overall 5-year survival rate of 0.4%. In many patients with pancreatic cancer, accurate preoperative diagnosis is difficult to achieve with conventional imaging analyses. Most patients with pancreatic cancer present late in the course of the disease and have either locally extensive or metastatic disease. Overall,
15 only up to 20% are candidates for resection and have the potential for curative surgery. Among the causes for this late presentation is the lack of diagnostic methods for an earlier detection of the disease. Besides this lack of diagnostic methods, the high mortality of patients with pancreatic cancer is additionally caused by a lack of effective treatments. Therefore, the identification of new targets for early diagnosis of pancreatic tumors, and
20 for the development of agents to treat pancreatic cancer is a challenge of paramount importance.

The problem of identifying polypeptides suitable as markers of pancreatic cancer
25 for early diagnosis of the disease, and the long felt need for such markers, was overcome by the present invention by applying the new technology of proteomics. It was surprisingly found by using proteomic technology that a specific set of polypeptides are differentially expressed in pancreatic tissue obtained from individuals suffering from
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pancreatic cancer, as compared to healthy pancreatic tissue. Said differentially expressed polypeptides are listed in appended tables 2 and 3. The polypeptides in table 3 are encoded by genes which were previously identified to be up-regulated in pancreatic cancer on the transcriptional level (Iacobuzio-Donahue et al., (2002), Am. J. Pathol. 160, 1239-1249). However, it is well known that regulation on the transcriptional level is not necessarily indicative of a similar regulation of the expression of the respective gene on the translational level. Thus, only by demonstrating that the polypeptides listed in table 3 are up-regulated in pancreatic cancer is it possible to use them for polypeptide-based diagnostic assays for the detection of pancreatic cancer.

10

Based on the polypeptides listed in tables 2 and 3, the present invention provides a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3 (Seq ID No. 1 to 24 and 26 to 49; and/or Seq ID No. 25 and 50 to 55). Thus, the term "marker" as used herein refers to one or more polypeptides that are regulated in cancer and that can be used to diagnose pancreatic cancer or a susceptibility to pancreatic cancer either alone or as combinations of multiple polypeptides that are known to be regulated in pancreatic cancer. Preferably, said polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48; and/or Seq ID No. 25 and 50 to 54. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15, 27, 31 to 35, 37, 39, 40; and/or Seq ID No. 50 to 52. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 and/or Seq ID No. 51 and 52. Most preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 14, 15 and 31; and/or Seq ID No. 52.

25

The term "polypeptide" as used herein, refers to a polymer of amino acids, and not to a specific length. Thus, peptides, oligopeptides and proteins are included within the definition of polypeptide.

30

Preferably, the marker of this invention is a marker comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 2.

Furthermore, a polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3, is used as a marker or as part of a marker for diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer. Preferably, said
5 polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48 from table 2 and/or Seq ID No. 25 and 50 to 54 from table 3. These polypeptides are induced at least two fold, as can be seen in tables 2 and 3. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15, 27, 31 to 35, 37, 39, 40 from table 2 and/or Seq ID No. 50
10 to 52 from table 3. These polypeptides are induced at least three fold, as can be seen in tables 2 and 3. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 from table 2 and/or Seq ID No. 51 and 52 from table 3. These polypeptides are induced at least 4 fold, as can be seen in tables 2 and 3. Most preferably, said polypeptides are selected from the group consisting
15 of Seq ID No. 4, 6, 14, 15 and 31 from table 2 and/or Seq ID No. 52 from table 3, which are the polypeptides that are induced five fold, as shown in tables 2 and 3.

The present invention pertains to a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the
20 polypeptides listed in table 6. Preferably, said at least one polypeptide additionally does not include Seq ID No.s 25 and 50 to 55.

In a preferred embodiment, the marker hereinbefore described additionally comprises at least one of the polypeptides listed in table 5.

25

Several groups of polypeptides were identified as markers for pancreatic cancers:

Enzymes

One of the enzymes that caught our attention was Glutamine γ -glutamyltransferase/tissue transglutaminase (TGLC, Seq ID No. 54). It is a member of the
30 transglutaminase family that catalyzes Ca^{2+} dependent reactions resulting in the post translational modification (cross-linking and conjugation with polyamines) of proteins at

the level of glutamine and lysine residues (Greenberg, C. S., Birckbichler, P. J., and Rice, R. H. Transglutaminases: multifunctional cross-linking enzymes that stabilize tissues. *FASEB J.*, 5: 3071-3077, 1991). Many different roles for this protein have been described, among them apoptosis, adhesion, and differentiation (Amendola, A., Fesus, L., Piacentini, M., and Szondy, Z. "Tissue" transglutaminase in AIDS. *J.Immunol.Methods*, 265: 145-159, 2002). There is some controversy on the role of TGLC in apoptosis. While several pieces of evidence suggest that TGLC is a pro-apoptotic protein (Melino, G., et al., *Mol.Cell Biol.*, 14: 6584-6596, 1994), Jason et al. found that TGLC acts in anti-apoptotic fashion (Boehm, J. E., et al. *J.Biol.Chem.*, 277: 20127-20130, 2002). Many substrates of TGLC are major extra-cellular matrix (ECM) components such as fibronectin, osteonectin, and collagen, which makes TGLC an important enzyme in ECM development (Raghunath, M., et al., *J.Clin.Invest*, 98: 1174-1184, 1996., Nemes, Z., Jr., et al. *J.Biol.Chem.*, 272: 20577-20583, 1997). Abnormal ECM development is involved in many pathological conditions such as fibrosis and may play a role in the proliferation of fibrous tissue observed in PC. Haroon et al. described that TGLC ECM-promoting abilities are an important part of the host response mechanism against tumor growth (Haroon, Z. A., et al., *Lab Invest*, 79: 1679-1686, 1999). Interestingly, loss of TGLC can be a biomarker for prostate adenocarcinoma (Birckbichler, P. J., et al., *Cancer*, 89: 412-423, 2000), which raises the question whether the measured TGLC is produced by neoplastic ductal cells and/or stromal cells. Measurements of mRNA levels in PC, normal tissue and PC cell lines indicate that TGLC is over expressed in both cell types (Iacobuzio-Donahue, C. A., et al., *Am.J.Pathol.*, 160: 1239-1249, 2002), which would distinguish PC from prostate adenocarcinoma.. Therefore, one preferred embodiment of the present invention is a marker comprising Seq ID No. 54.

25 Cytoskeletal proteins

Several cytoskeletal proteins were detected at higher levels in PC than in surrounding tissue. One of these is gelsolin (Seq ID No. 3), a Ca^{2+} and PIP2 (polyphosphoinositide 4,5-bisphosphate) regulated severing and capping protein, which is a multifunctional actin regulatory protein and has roles in actin remodeling, motility, signaling, apoptosis and cancer (Maruta, H. G proteins cytoskeleton and cancer. Austin, Tex.: R.G. Landes, 1998). In several cancer studies, gelsolin expression has been described as down-regulated during carcinogenesis (breast, colon, stomach, bladder, prostate, and lung) (Asch, H. L., et al., *Cancer Res.*, 56: 4841-4845, 1996; Dosaka-Akita, H., et al., *Cancer Res.*, 58: 322-327, 1998, Prasad, S. C., et al. *Electrophoresis*, 18: 629-637, 1997). Another example for an up-regulated cytoskeletal protein is fascin (Seq ID No. 58), an

actin-bundling protein that has a role in cell matrix adhesion, cell interaction and migration. Fascin over expression has been reported in several cancers, such as breast, colon, and ovarian carcinoma (29). The present invention also features fascin 2 as a polypeptide up-regulated in pancreatic cancer (Seq ID No. 56). Thus, a preferred
5 embodiment of the present invention is a marker comprising Seq ID. No. 3. In another preferred embodiment, the marker comprises Seq. ID No. 58. In another preferred embodiment, the marker comprises Seq. ID No. 56.

In our study, cytokeratin 7 (Seq. ID No. 52) and cytokeratin 19 (Seq ID No. 33) showed strong expression in PC. Both have also been described in other cancers and have
10 been linked with metastasis formation (Moll, R., *Int.J.Biol.Markers*, 9: 63-69, 1994.). High protein levels of actinin-4 (Seq ID No. 5) were detected in PC. This protein was linked by others with cell motility and cancer invasion (Honda, K., Yamada, T., Endo, R., Ino, Y., Gotoh, M., Tsuda, H., Yamada, Y., Chiba, H., and Hirohashi, S. *J.Cell Biol.*, 140: 1383-1393, 1998.). Taken together, the apparent strong expression of cytoskeletal
15 proteins is likely to be an important factor in the strong invasiveness and metastasis-forming potential of PC. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 52. In another preferred embodiment, the marker comprises Seq. ID No. 33. In another preferred embodiment, the marker comprises Seq. ID No. 5.

20 Metastasis

Cancer of exocrine pancreas is characterized by extensive local invasion, early lymphatic and hematogenous metastasis. Metastasis in PC has been found in the skeleton, eye, bladder, etc. The extent of angiogenesis depends on the balance between pro-angiogenic or anti-angiogenic factors released from cancer and host cell. Currently,
25 intratumoral microvessel density (IMD) measured by immunocytochemistry appears to be the most reliable parameter for assessing angiogenic activity. Patients with high IMD have decreased survival rates in a variety of cancers (Fujioka, S., et al., *Cancer*, 92: 1788-1797, 2001). Thymidine phosphorylase (TYPH or TP, Seq ID No. 31) which is identical to platelet-derived endothelial cell growth factor, is strongly expressed in PC and
30 stimulates the chemotaxis of endothelial cells through the 2-deoxy-D-ribose, degradation products of thymidine by TP, thus indirectly inducing angiogenesis (Haraguchi, M., et al. *Nature*, 368: 198, 1994.). Shuichi Fujioka et al. found that IMD and TP status were independent predictive indicators for overall as well as relapse-free survival in PC (Fujioka, S., et al., *Cancer*, 92: 1788-1797, 2001). An additional protein detected at higher
35 levels in PC than in surrounding tissue likely involved in metastasis formation is

osteoblast specific factor 2 (Seq ID No.53), a putative bone adhesion protein. Breast carcinoma commonly metastasizes to bone (Guise, T. A. Cancer, 88: 2892-2898, 2000). Although the role of this protein in PC is not clearly established, our findings suggest a similar role for osteoblast specific factor 2 in PC. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 31. In another preferred embodiment, the marker comprises Seq. ID No. 53.

Small GTP-binding proteins

Four small GTP-binding proteins and interacting proteins were more strongly expressed in PC than in normal pancreas tissue. These include RAN (Seq. ID No. 27), GBLP (guanine nucleotide binding protein β subunit-like protein RACK1, Seq. ID No. 47), GDIR (Rho GDP dissociation inhibitor 1, Seq. ID No. 55), and IQG1 or IQGAP1 (Ras gtpase activating like protein, Seq ID No. 25). Small GTP-binding proteins constitute a superfamily, which is structurally classified into at least five families: the Ras, Rho, Rab, Sar1/Arf, and Ran families and are involved in the regulation of gene expression, cytoskeletal reorganization, and nucleocytoplasmic transport (Takai, Y., et al. Physiol Rev., 81: 153-208, 2001). RAN is known to enhance androgen receptor-mediated transactivation and was shown to be overexpressed in prostate cancer (Sampson, E. R., et al., J.Biol.Regul.Homeost.Agents, 15: 123-129, 2001). Increased expression of RAN in 81% of prostate tumor cases, may contribute to over proliferation of prostate tumor cells (Li, P., et al., Am J Pathol., 161: 1467-1474,2002). GBLP is an anchoring protein for activated protein kinase C β and a variety of other proteins. Protein kinase C plays an important role in angiogenesis and cancer growth. Berns et al. found GBLP up-regulated in during angiogenesis *in vitro* and also associated with nonendothelial cells in angiogenically active tissue (Berns, H., et al., FASEB J., 14: 2549-2558, 2000). Further more, mRNA expression of GBLP is detected in epithelial cells of human colon carcinoma and proliferating epithelial cell of normal colon tissue. Therefore, there is a likely link between high GBLP expression and tumor growth. GDIR (Rho GDP dissociation inhibitor) had been found up-regulated in a chemoresistant fibrosarcoma cell line by 2D-PAGE (Sinha, P., et al., Electrophoresis, 20: 2961-2969, 1999) and may block apoptotic signal pathway mediated by Ras and c-jun kinase, resulting in the increase resistance against environmental stress. IQG1 (Ras GTPase-activating-like protein) is a widely expressed 190-kDa Cdc42-, Rac1-, and calmodulin-binding protein that interacts with F-actin *in vivo* and that can cross-link F-actin microfilaments *in vitro*. IQG1 negatively regulates the Ecc-based (E-cadherin/catenin complex) cell-cell adhesion by dissociating alpha-catenin. Up-regulation of IQGAP1 is correlated with the malignant

phenotype in gastric cancer (Sugimoto, N., et al., *J. Hum. Genet.*, 46: 21-25, 2001). By immunohistochemical analysis, IQGAP1 was found overexpressed in colorectal carcinoma and associated with carcinoma invasion (Nabeshima, K., et al., *Cancer Lett.*, 176: 101-109, 2002). Since cancer invasiveness is associated with the localized disruption of cell-cell adhesion, both our results and Iacobuzio-Donahue et al.'s data suggest that IQGAP1 may be involved in the disruption of local adhesion and in PC invasion to surrounding tissue. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 27. In another preferred embodiment, the marker comprises Seq. ID No. 47. In another preferred embodiment, the marker comprises Seq. ID No. 55. In another preferred embodiment, the marker comprises Seq. ID No. 25.

S100 protein family

Another protein with high-level expression in PC is S109 (S100A9, MRP-14, calgranulin B, Seq ID No. 49), a member of the S100 protein family of highly homologous low molecular weight calcium binding proteins. Calgranulins are characterized by cell type-specific expression in cells of epithelial, myeloid and endothelial origin and accumulation at sites of acute and chronic inflammation (e.g. rheumatoid arthritis, cystic fibrosis, psoriasis, allergic dermatitis, inflammatory bowel diseases) (Donato, R. *Int.J.Biochem.Cell Biol.*, 33: 637-668, 2001). S100A8 and S100A9 can form a noncovalent heterodimer protein complex called calprotectin. Current reports support that both of S100A9 and S100 A8 have wide range of possible intracellular as well as extracellular functions (Schafer, B. W. and Heizmann, C. W. *Trends Biochem.Sci.*, 21: 134-140, 1996). S100A8 and S100A9 are negatively regulated by glucocorticoids in a c-Fos-dependent manner and over expressed throughout skin carcinogenesis (Gebhardt, C., et al., *Oncogene*, 21: 4266-4276, 2002). These proteins are also more strongly expressed in colorectal carcinoma than in matched normal colon mucosa, as shown by proteomics analysis (Stulik, J., et al., *Electrophoresis*, 20: 1047-1054, 1999). S100A9 has been detected in cultured human adenocarcinoma (AC) cells derived from various organs, and is associated with tumor differentiation in pulmonary adenocarcinoma (Arai, K., et al., *Oncol.Rep.*, 8: 591-596, 2001). Iacobuzio-Donahue et al.'s work indicates that over expression of S100A4 in PC is associated with poor differentiation and DNA hypomethylation (Rosty, C., et al., *Am.J.Pathol.*, 160: 45-50, 2002). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 49.

Annexin

We found that annexin 1 (Seq ID No. 51) and annexin 2 (Seq ID No. 19) have high level of expression in PC. Both are members of a family of Ca^{2+} -dependent membrane-binding proteins. Described functions include, among others, an important role in malignant transformation (Masaki, T., et al., *Hepatology*, 24: 72-81, 1996), the control of epithelial cell line proliferation (Solito, E., et al., *Cell Growth Differ.*, 9: 327-336, 1998), and mediation of apoptosis (Canaider, S., et al., *Life Sci.*, 66: L265-L270, 2000). Evidence in support of causative roles for any annexins in the development of cancer is still mainly circumstantial. In MCF-7 breast carcinoma cells, overexpression of annexin1 led to abrogation of Ca^{2+} release after activation of purinergic or bradykinin receptors (Frey, B. M., et al., *FASEB J.*, 13: 2235-2245, 1999), while over expression of annexin1 in rat 2 fibroblasts leads to direct inhibition of cytosolic PLA2, which in turn depresses the serum response element of c-fos (Oh, J., et al., *FEBS Lett.*, 477: 244-248, 2000). Collectively, these studies imply a growth-suppressive role for annexin1. These results are not supported by the finding that annexin 1 is strongly up-regulated in a prostate cancer cell line (Vaarala, M. H., *Lab Invest*, 80: 1259-1268, 2000), esophageal cancer (Emmert-Buck, M. R., et al., *Mol.Carcinog.*, 27: 158-165, 2000), a stomach cancer cell line (Sinha, P., et al., *J.Biochem.Biophys.Methods*, 37: 105-116, 1998), mammary adenocarcinoma (Pencil, S. D. and Toth, M. *Clin.Exp.Metastasis*, 16: 113-121, 1998), and hepatocarcinoma (de Coupade, C., et al., *Hepatology*, 31: 371-380, 2000). In hepatocarcinoma, study also showed that the proliferative rate of both normal and malignant hepatocytes was attenuated by antisense to annexin 1. These and our data suggest that cell growth is associated with elevated rather than reduced levels of annexin 1, which is also supported by the studies of Iacobuzio- Donahue et al. (*Am. J. Pathol.*, 160: 1239-1249, 2002). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 51. In another preferred embodiment, the marker comprises Seq. ID No. 19.

Some additional proteins highly expressed in PC may have either clear roles in PC or an indirect link with PC, e.g. BGH3 (TGF- β 1-induced protein, Seq ID No. 6) which is a secretory protein and acts as a marker for biologically active TGF- β 1 (Langham, R. G., et al., *Transplantation*, 72: 1826-1829, 2001). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 6.

With the identification of polypeptides regulated in pancreatic cancer, the present invention provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of obtaining a biological sample; and detecting and/or measuring the increase of a marker described hereinbefore. The term "detection" as used herein refers to the qualitative determination of the absence or presence of polypeptides. The term "measured" as used herein refers to the quantitative determination of the differences in expression of polypeptides in biological samples from patients with pancreatic cancer and biological samples from healthy individuals. Methods for detection and/or measurement of polypeptides in biological samples are well known in the art and include, but are not limited to, Western-blotting, ELISAs or RIAs. Antibodies recognizing the polypeptides listed in table 2, 3, 5 and/or 6 can either be generated for the purpose of detecting said polypeptides, eg. by immunizing rabbits with purified proteins, or known antibodies recognizing said polypeptides can be used. For example, an antibody capable of binding to the denatured proteins, such as a polyclonal antibody, can be used to detect the peptides of this invention in a Western Blot. An example for a method to measure a marker is an ELISA. This type of protein quantitation is based on an antibody capable of capturing a specific antigen, and a second antibody capable of detecting the captured antigen. A further method for the detection of a diagnostic marker for pancreatic cancer is by analysing biopsy specimens for the presence or absence of the markers of this invention. Methods for the detection of these markers are well known in the art and include, but are not limited to, immunohistochemistry or immunofluorescent detection of the presence or absence of the polypeptides of the marker of this invention. Methods for preparation and use of antibodies, and the assays mentioned hereinbefore are described in Harlow, E. and Lane, D. Antibodies: A Laboratory Manual, (1988), Cold Spring Harbor Laboratory Press.

The accuracy of the diagnosis of pancreatic cancer can be increased by analysing combinations of multiple polypeptides listed in tables table 2, 3, 5 and/or 6. Thus, the in vitro method herein before described, comprises a marker which comprises at least two, preferably at least three, more preferably at least four, even more preferably at least five, and most preferably at least six of the polypeptides listed in table 2,3, 5 and/or 6.

For diagnosis of pancreatic cancer, suitable biological samples need to be analysed for the presence or absence of a marker. Said biological samples can be serum, plasma,

pancreatic juice or cells of pancreatic tissue. Cells from pancreatic tissue can be obtained by ERCP, secretin stimulation, fine-needle aspiration, cytologic brushings and large-bore needle biopsy.

- 5 It is also possible to diagnose pancreatic cancer by detecting and/or measuring nucleic acid molecules coding for the marker hereinbefore described. Preferably, said nucleic acid molecule is RNA or DNA. In another embodiment, said DNA is a cDNA.

- 10 In one embodiment of the present invention, the in vitro method herein before described comprises comparing the expression levels of at least two of the nucleic acids encoding said polypeptides in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer, to the expression levels of the same nucleic acids in a healthy individual.

- 15 In another embodiment of the present invention the in vitro method herein before described comprises comparing the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer to the expression levels of the same marker in a healthy individual. In a more preferred embodiment of the in vitro method, an increase or decrease of the expression levels of
20 said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

- The present invention also provides a screening method for identifying and/or obtaining a compound which interacts with a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of contacting
25 said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and detecting the interaction between said compound or plurality of compounds with said polypeptide.

- The "interaction" in the screening methods as disclosed herein may be measured by
30 conventional methods. The type of conventional method for testing the interaction of a

compound with a polypeptide that is soluble, as opposed to membrane associated, can be an in vitro method using either purified recombinant polypeptide, or native polypeptide purified from cells that endogenously express the polypeptide. As a non-limiting example, a polypeptide of the invention can be bound to beads or immobilized on plastic or other surfaces, and interaction of a compound with the polypeptide can be measured by either using a labelled compound and measuring the label bound to the polypeptide or by displacement of a labeled known ligand from said polypeptide.

For polypeptides that are associated with the cell membrane on the cell surface, or which are expressed as transmembrane or integral membrane polypeptides, the interaction of a compound with said polypeptides can be detected with different methods which include, but are not limited to, methods using cells that either normally express the polypeptide or in which the polypeptide is overexpressed, eg. by detecting displacement of a known ligand which is labeled by the compound to be screened. Alternatively, membrane preparations may be used to test for interaction of a compound with such a polypeptide

Interaction assays to be employed in the method disclosed herein may comprise FRET-assays (fluorescence resonance energy transfer; as described, inter alia, in Ng, Science 283 (1999), 2085-2089 or Ubarretxena-Belandia, Biochem. 38 (1999), 7398-7405), TR-FRETs and biochemical assays as disclosed herein. Furthermore, commercial assays like "Amplified Luminescent Proximity Homogenous AssayTM" (BioSignal Packard) may be employed. Further methods are well known in the art and, inter alia, described in Fernandez, Curr. Opin. Chem. Biol. 2 (1998), 547-603.

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The "test for interaction" may also be carried out by specific immunological and/or biochemical assays which are well known in the art and which comprise, e.g., homogenous and heterogenous assays as described herein below. Said interaction assays employing read-out systems are well known in the art and comprise, inter alia, two-hybrid screenings (as, described, inter alia, in EP-0 963 376, WO 98/25947, WO 00/02911; and as exemplified in the appended examples), GST-pull-down columns, co-precipitation assays from cell extracts as described, inter alia, in Kasus-Jacobi, Oncogene 19 (2000), 2052-2059, "interaction-trap" systems (as described, inter alia, in US

6,004,746) expression cloning (e.g. lamda gt11), phage display (as described, inter alia, in US 5,541,109), in vitro binding assays and the like. Further interaction assay methods and corresponding read out systems are, inter alia, described in US 5,525,490, WO 99/51741, WO 00/17221, WO 00/14271 or WO 00/05410. Vidal and Legrain (1999) in Nucleic
5 Acids Research 27, 919-929 describe, review and summarize further interaction assays known in the art which may be employed in accordance with the present invention.

Homogeneous (interaction) assays comprise assays wherein the binding partners remain in solution and comprise assays, like agglutination assays.
10 Heterogeneous assays comprise assays like, inter alia, immuno assays, for example, Enzyme Linked Immunosorbent Assays (ELISA), Radioactive Immunoassays (RIA), Immuno Radiometric Assays (IRMA), Flow Injection Analysis (FIA), Flow Activated Cell Sorting (FACS), Chemiluminescent Immuno Assays (CLIA) or Electrogenerated Chemiluminescent (ECL) reporting.

15

The present invention further provides a screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting said polypeptide with a compound identified and/or obtained by
20 the screening method described above under conditions which allow interaction of said compound with said polypeptide; b) determining the activity of said polypeptide; c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison
25 to (c) is indicative for an inhibitor or antagonist. The terms inhibitors and antagonists as used herein are used interchangeably. This screening assay can be performed either as an in vitro assay, or as a host-based assay. The host to be employed in the screening methods of the present invention and comprising and/or expressing a polypeptide listed in table 2, 3, 5 and/or 6 may comprise prokaryotic as well as eukaryotic cells. Said cells may
30 comprise bacterial cells, yeast cells, as well as cultured (tissue) cell lines, inter alia, derived from mammals. Furthermore animals may also be employed as hosts, for example a non-human transgenic animal. Accordingly, said host (cell) may be transfected or transformed with the vector comprising a nucleic acid molecule coding for a polypeptide which is differentially regulated in pancreatic cancer as disclosed herein. Said host cell or
35 host may therefore be genetically modified with a nucleic acid molecule encoding such a

polypeptide or with a vector comprising such a nucleic acid molecule. The term "genetically modified" means that the host cell or host comprises in addition to its natural genome a nucleic acid molecule or vector coding for a polypeptide listed in table 2, 3, 5 and/or 6 or at least a fragment thereof. Said additional genetic material may be introduced
5 into the host (cell) or into one of its predecessors/parents. The nucleic acid molecule or vector may be present in the genetically modified host cell or host either as an independent molecule outside the genome, preferably as a molecule which is capable of replication, or it may be stably integrated into the genome of the host cell or host.

10 As mentioned herein above, the host cell of the present invention may be any prokaryotic or eukaryotic cell. Suitable prokaryotic cells are those generally used for cloning like *E. coli* or *Bacillus subtilis*. Yet, these prokaryotic host cells are also envisaged in the screening methods disclosed herein. Furthermore, eukaryotic cells comprise, for example, fungal or animal cells. Examples for suitable fungal cells are yeast cells,
15 preferably those of the genus *Saccharomyces* and most preferably those of the species *Saccharomyces cerevisiae*. Suitable animal cells are, for instance, insect cells, vertebrate cells, preferably mammalian cells, such as e.g. CHO, HeLa, NIH3T3 or MOLT-4. Further suitable cell lines known in the art are obtainable from cell line depositories, like the American Type Culture Collection (ATCC).

20 The hosts may also be selected from non-human mammals, most preferably mice, rats, sheep, calves, dogs, monkeys or apes. As described herein above, said animals/mammals also comprise non-human transgenic animals, which preferably express at least one polypeptide differentially regulated in pancreatic cancer as disclosed
25 herein. Preferably, said polypeptide is a polypeptide which is up-regulated in tissue derived from patients with pancreatic cancer. Yet it is also envisaged that non-human transgenic animals be produced which do not express marker genes as disclosed herein or who express limited amounts of said marker gene products. Said animals are preferably related to polypeptides which are down-regulated in pancreatic cancer. Transgenic non-
30 human animals comprising and/or expressing the up-regulated polypeptides of the present invention or alternatively, which comprise silenced or less efficient versions of down-regulated polypeptides are useful models for studying the development of pancreatic cancer and provide for useful models for testing drugs and therapeutics for pancreatic cancer treatment and/or prevention.

A compound which interacts with a polypeptide listed in table 2, 3, 5 and/or 6 and which inhibits or antagonizes said polypeptide is identified by determining the activity of said polypeptide in the presence of said compound.

5 The term "activity" as used herein relates to the functional property or properties of a specific polypeptide. For the enzymes listed in table 2, 3, 5 and/or 6, the term "activity" relates to the enzymatic activity of a specific polypeptide. Activity assays for the enzymes listed in table 2, 3, 5 and/or 6 are well known.

10 For adhesion molecules listed in table 2, 3, 5 and/or 6, the term "activity" relates to the adhesive properties of a polypeptide and may be determined using assays such as, but not limited to, adhesion assays, cell spreading assays, or in vitro interaction of the adhesion molecule with a known ligand. Such assays are well known in the art.

15 For cytoskeletal proteins, the term "activity" relates to the regulation of the cytoskeleton by such polypeptides, or to their incorporation into the cytoskeleton. As a non-limiting example, the ability of Gelsolin to regulate actin polymerization, or of Filamin A to promote orthogonal branching of actin filaments, may be determined using in vitro actin polymerization assays. Activity in relation to the regulation of cytoskeletal
20 structures may further be determined by, as non-limiting examples, cell spreading assays, cell migration assays, cell proliferation assays or immunofluorescence assays, or by staining actin filaments with fluorescently labeled phalloidin. All of these assays are well known to the person skilled in the art.

25 For ion channels (Chloride intracellular channel protein) the term "activity" relates to ion flux (Chloride flux) across the membrane. Methods to determine ion flux across membranes are well known to the person skilled in the art.

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For transcription factors, eg. KIAA 1034, the term "activity" relates to their ability to regulate gene transcription. The transcriptional activity of a polypeptide can be determined using commonly used assays, such as a reporter gene assay.

5 For growth factors and hormones or their receptors, the term "activity" relates to their ability to bind to their receptors or ligands, respectively, and to induce receptor activation and subsequent signaling cascades, and/or it relates to the factor's or receptor's ability to mediate the cellular function or functions eventually caused by growth factor or hormone mediated receptor activation. Growth factor or hormone binding to receptors
10 can be determined by commonly known ligand binding assays. Receptor activation can be determined by testing for receptor auto-phosphorylation, or by assaying for modification or recruitment of downstream signaling mediators to the receptors (by immunoprecipitation and Western Blotting of signaling complexes). Cellular functions regulated by growth factors or hormones and their receptors can be cell proliferation (eg
15 determined by using thymidine incorporation or cell counts), cell migration assays (eg determined by using modified Boyden chambers), cell survival or apoptosis assays (eg determined by using DAPI staining), angiogenesis assays (eg in vitro assays to measure endothelial tube formation that are commercially available). In addition to these assays, other assays may be used as well to determine these and other cellular functions.

20

Inhibitors or antagonists of a polypeptide listed in tables 2 and/or 3 are identified by the screening method described above when there is a decreased activity determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor or antagonist.

25

Further to the screening methods disclosed above, this invention provides a screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting a host which expresses said
30 polypeptide with a compound; b) determining the expression level and/or activity of said polypeptide; c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the expression level of said polypeptide as determined in (b) and

(c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

5 An inhibitor of the expression of a polypeptide listed in table 2, 3, 5 and/or 6 is identified by the screening method described hereinbefore when a decreased expression of the protein is determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor of expression of a polypeptide.

10 The term "express" as used herein relates to expression levels of a polypeptide listed table 2, 3, 5 and/or 6 which is up-regulated in pancreatic cancer, in cells, preferably in a pancreatic adenocarcinoma cell line, which are elevated as compared to the expression levels of the same polypeptide in healthy pancreatic cells. Preferably, expression levels are at least 2 fold, more preferably at least 3 fold, even more preferably
15 at least 4 fold, most preferably at least 5 fold higher than in healthy pancreatic cells.

Furthermore, the present invention provides a compound identified and/or obtained by any of the screening methods hereinbefore described. Said compound is further comprised in a pharmaceutical composition. A method for the preparation of
20 said pharmaceutical composition comprising formulating said compound in a pharmaceutically acceptable carrier or diluent is also claimed. Any conventional carrier material can be utilized. The carrier material can be an organic or inorganic one suitable for eteral, percutaneous or parenteral administration. Suitable carriers include water, gelatin, gum arabic, lactose, starch, magnesium stearate, talc, vegetable oils, polyalkylene-
25 glycols, petroleum jelly and the like. Furthermore, the pharmaceutical preparations may contain other pharmaceutically active agents. Additional additives such as flavoring agents, stabilizers, emulsifying agents, buffers and the like may be added in accordance with accepted practices of pharmaceutical compounding.

30 Said compound may be used for the preparation of a medicament for the treatment or prevention of pancreatic cancer. In addition, said compound may also be used for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. Preferably, said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense
35 construct.

Within the scope of the present invention, antibodies against the proteins listed in tables 2 and/or 3, or antigen-binding fragments thereof, may be used in an in vitro method for the diagnosis of pancreatic cancer.

5 In order to efficiently perform diagnostic screenings, the present invention provides a kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, described above. Another kit provided by this invention is a kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker hereinbefore described. Yet another kit provided
10 by this invention is a kit for screening of compounds that antagonize any of the polypeptides listed in tables 2 and/or 3 or inhibit the expression of any of said polypeptides.

The present invention pertains to a marker for diagnosis of pancreatic cancer
15 comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6. Preferably, said marker does not include Seq ID No.s 25 and 50 to 55. In a more preferred embodiment, said marker comprises at least one of the polypeptides listed in table 5.

The present invention also provides an in vitro method for the diagnosis of
20 pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

- a) obtaining a biological sample; and
- b) detecting and/or measuring the increase of at least one of the polypeptides listed in table 6.

Preferably, said in vitro method additionally comprises the step of detecting and/or
25 measuring the decrease of at least one of the polypeptides listed in table 5. More preferably, in said vitro method, said at least one polypeptide does not include Seq ID No.s 25 and 50 to 55. Even more preferably, in said vitro method, said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.

30

The present invention further provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

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a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker hereinbefore described.

Preferably, in said in vitro method, said nucleic acid molecule is RNA or DNA.

5 More preferably, in said in vitro method, said DNA is a cDNA.

In a further more preferred embodiment of any of the in vitro methods hereinbefore described, the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual. In a most preferred embodiment of any of the in vitro methods hereinbefore described, the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

In a further preferred embodiment of the in vitro method hereinbefore described, an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

The present invention also pertains to a screening method for identifying and/or obtaining a compound which interacts with a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

Furthermore, the present invention provides a screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

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- a) contacting said polypeptide with a compound identified and/or obtained by the screening method of claim 39 under conditions which allow interaction of said compound with said polypeptide;
- b) determining the activity of said polypeptide;
- 5 c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and
- d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.

10

The present invention also provides a screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

15

- a) contacting a host which expresses said polypeptide with a compound,
- b) determining the expression level and/or activity of said polypeptide;
- c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and
- 20 d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

The present invention provides a compound identified and/or obtained by the
25 screening methods hereinbefore described.

In addition, the present invention provides a pharmaceutical composition comprising the compound hereinbefore described. Also provided is a method for the preparation of the pharmaceutical composition hereinbefore described comprising
30 formulating the compound hereinbefore described in a pharmaceutically acceptable carrier or diluent.

- 20 -

The present invention provides a use of a compound hereinbefore described for the preparation of a medicament for the treatment or prevention of pancreatic cancer. Also provided is a use of a compound hereinbefore described for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. In a preferred embodiment, the uses hereinbefore described relate to a compound comprising an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

Within the scope of the present invention, antibodies against the proteins listed in tables 5 and/or 6, or antigen-binding fragments thereof, may be used in an in vitro method for the diagnosis of pancreatic cancer.

In order to efficiently perform diagnostic screenings, the present invention provides a kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, described above. Another kit provided by this invention is a kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker hereinbefore described. Yet another kit provided by this invention is a kit for screening of compounds that antagonize any of the polypeptides listed in tables 5 and/or 6 or inhibit the expression of any of said polypeptides.

In the present invention, the proteins, compounds, kits, methods and uses substantially as herein before described, especially with reference to the foregoing examples are also claimed.

Examples:

Collection of tissue samples

- 5 Pancreatic carcinomas and adjacent tissue were collected from the patients listed in table 1.

Samples were collected shortly after the resection (less than 30 minutes), and fast frozen in liquid nitrogen for about 1 minute, then stored in a freezer at a temperature of -80°C .

10 Characterization of formalin-fixed specimens

Histopathological characterization was carried out by using hematoxylin-eosin-stained sections of formalin-fixed and paraffin-embedded specimens. Tumors were classified using the WHO system. The types of pancreatic carcinomas included in the study are shown in table 1.

15

- 20 The twelve pancreatic carcinoma samples used in this study were ductal carcinomas which constitute the overwhelming proportion of pancreatic carcinomas. The patient-matched samples from histologically normal tissue surrounding the carcinoma were used as controls. We carried out 12 pairs of 2-dimensional electrophoresis maps for comparing protein expression between tumor tissue and normal control tissue. For protein identification, the samples were pooled, thus generating pan-Carcinoma and pan-Normal protein extracts. Quantification was carried out in two steps: (I) Gels from the pooled samples were compared using the PDQuest image analysis software. (II) The changes identified at the level of the pooled samples were cross-validated by an analysis of the individual samples. The change factors shown in table 2, 3, 5 and 6 were determined using the pooled samples.
- 25

Preparation of samples for electrophoresis

Samples cleaned of clots and contaminating tissue were frozen in liquid nitrogen, then ground to powder. Samples were suspended in lysis buffer (8M urea, 4% CHAPS, 40mMol/L Tris-Cl, 0.5% carrier ampholytes, 100mMol/L DTT and 0.1g/l PMSF) and
5 centrifuged at 12000rpm for 30 minutes. The supernatants were stored at -80°C. The protein concentration in the extracts was determined by the Bradford method (Bradford, M. Anal. Biochem. 72, 248 (1976)).

Two-dimensional gel electrophoresis

10 Samples containing 1 mg of protein were loaded onto the rehydrated IPG strip (18 cm, pH3~10) by using the cup loading method. IEF was performed using Pharmacia Multiphor apparatuses under the following conditions: First, the voltage was increased 200V-5000V over 24hrs, then a constant voltage of 5000V was applied for 24 hrs, the running temperature was 20°C. After IEF, the strips were equilibrated with 10 ml
15 equilibration solution I (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 30 mM Dithioerythritol) for 15 min, then for another 15 min with equilibration solution II (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 0.23 M Iodoacetamide).

The second dimension SDS polyacrylamide gel electrophoresis (SDS-PAGE) was
20 carried out using a Hoefer ISO_DALT apparatus (10 gels/run, 24×20 cm), IEF strips were loaded onto 12% homogeneous polyacrylamide gels (1.5 mm x 24 cm x 20 cm). The gels were run in TGS_Buffer (250 mM Tris, 1.92 M Glycine, 1% (w/v) SDS, pH = 8.3, Bio-Rad) at a constant voltage (80 V, 20°C).

25 Gel fixation and staining

Gels were fixed in 50% Methanol/20% acetic acid for 30 min, then washed in ultra-pure water for 30 min and stained with NOVEX Colloidal Blue staining Kit (Invitrogen) following the manufacturer's recommendations.

Protein Identification

The protein identification was performed using a two-step procedure.

In-gel digestion

- 5 Spots were picked and transferred into 96-well by a spot picking robot. From each gel, 600-800 spots were picked. The spots were destained with 100µl of 30% acetonitrile in 50mM ammonium bicarbonate, washed in ultra pure-water and dried in a speed vac evaporator. The dry gel pieces were digested with 10ng/µl trypsin (Promega, Madison, USA) solution in 500 nM ammonium bicarbonate at room temperature for 16 h
- 10 maximum. The peptides from each spot were extracted with 20µl of 0.1% trifluore acetic acid (TFA) in 50% acetonitrile. The matrix solution consisted of 0.025%(w/v) alfa-cyano-4-hydroxy cinammic acid (Sigma) in 50% acetonitrile/0.1% TFA with internal standard peptides des-Arg-Bradykinin(Sigma, MW 904.4681 Da) and adrenocorticotrophic hormone fragment 18-39 (Sigma, MW 2465.1989 Da).

15

Analysis by MALDI-TOF

- 1.5µl of peptide extract and 1.0µl of matrix solution were stimulaniously applied to the spots on the MS target. Recrystallization was carried out as specified by the instruments manufacturer. The samples were analyzed in a MALDI-time of flight Mass spectrometer (Autoflex, Bruker Analytics, Bremen, Germany). Peak annotation and
- 20 database search by peptide matching was performed by in house developed software. The peptide mass was compared with theoretic peptide masses of all available proteins from all species. The monoisotopic mass was used and a mass tolerance of 0.0025% was allowed. 4 matching peptides were the minimal requirement for an identity assignment.
- 25 Mismatch or miscleavage sites were not considered.

Table 1: Clinical and histopathological characteristics of samples

No. of Samples	Sex	Age	Tumor location	Histology	Metastasis in lymph nodes
PC-01	Male	48	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-02	Male	68	Head of pancreas	Poorly differentiated adenocarcinoma	Yes
PC-03	Male	44	Head of pancreas	Poorly differentiated ductal adenocarcinoma, clear cell type	Yes
PC-04	Male	66	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-05	Female	45	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-06	Female	65	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-07	Male	59	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-08	Female	62	Body of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-09	Male	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	No
PC-10	Female	53	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-11	Female	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-12	Female	69	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes

Table 2: Proteins up-regulated in pancreatic cancer I

Protein	Acc No	Description	Seq ID No.	Fold Change
sw:CATD_HUMAN	P07339	Cathepsin D precursor (ec 3.4.23.5).	1	<2
sw:IDHC_HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (ec 1.1.1.42)	2	2
sw:GELS_HUMAN	P06396	Gelsolin precursor, plasma	3	3
sw:CFAB_HUMAN	P00751	Complement factor B precursor (ec 3.4.21.47)	4	5
sw:AAC4_HUMAN	O43707	Alpha-actinin 4 (non-muscle alpha-actinin 4)	5	2
sw:AAC1_HUMAN	P12814	Alpha-actinin 1 (alpha-actinin cytoskeletal isoform)	7	2
sw:TBA4_HUMAN	P05215	Tubulin alpha-4 chain.	8	2
sw:ABP2_HUMAN	P21333	Filamin A (Endothelial actin-binding protein)	9	4
sw:TAGL_HUMAN	P37802	Transgelin 2 (smooth muscle protein 22-alpha)	10	2
sw:TPM4_HUMAN	P07226	Tropomyosin alpha 4 chain	11	<2
sw:BGH3_HUMAN	Q15582	Transforming growth factor-beta induced protein IG-H3 precursor	6	5
sw:CALD_HUMAN	Q05682	Caldesmon (cdm)	12	2
sw:ENOL_HUMAN	Q05524	Alpha enolase	13	2
sw:ACY1_HUMAN	Q03154	Aminoacylase-1	14	5
sw:CAPB_HUMAN	P47756	F-actin capping protein beta subunit (capz beta)	15	5
sw:IPYR_HUMAN	Q15181	Inorganic pyrophosphatase	16	<2
sw:LEG3_HUMAN	P17931	Galectin-3 (galactose-specific lectin 3).	17	2

sw:POR2_HUMAN	P45880	Voltage-dependent anion-selective channel protein 2	18	<2
SW:ANX2_HUMAN	P07355	Annexin II	19	2
sw:CBP2_HUMAN	P50454	Collagen-binding protein 2 precursor	20	2
sw:COF1_HUMAN	P23528	Cofilin, non-muscle isoform	21	<2
sw:CYPH_HUMAN	P05092	Peptidyl-prolyl cis-trans isomerase A	22	<2
sw:DYI2_HUMAN	Q13409	Dynein intermediate chain 2, cytosolic	23	2
sw:ECH1_HUMAN	Q13011	Delta3,5-Delta2,4-dienoyl-coa isomerase, mitochondrial precursor	24	2
sw:MLRN_HUMAN	P24844	Myosin regulatory light chain 2	48	2
sw:PLSL_HUMAN	P13796	L-Plastin	26	<2
sw:RAN_HUMAN	P17080	GTP-binding nuclear protein ran	27	3
sw:ROK_HUMAN	Q07244	Heterogeneous nuclear ribonucleoprotein k	28	2
sw:TCTP_HUMAN	P13693	Translationally controlled tumor	29	<2
sw:TPM1_HUMAN	P09493	Tropomyosin 1 alpha chain	30	<2
sw:TYPH_HUMAN	P19971	Thymidine phosphorylase precursor	31	5
sw:AMPL_HUMAN	P28838	Cytosol aminopeptidase	32	3
sw:K1CS_HUMAN	P08727	Keratin, type i cytoskeletal 19 (cytokeratin 19)	33	4
sw:ALDX_HUMAN	P14550	Alcohol dehydrogenase [NADP+]	34	4
sw:EL3A_HUMAN	P09093	Elastase IIIa precursor	35	4
sw:DLDH_HUMAN	P09622	Dihydrolipoamide dehydrogenase, mitochondrial precursor	36	2
sw:ECHM_HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial precursor	37	3
sw:HSBX_HUMAN	O14558	Heat-shock 20 kDa like-protein p20.	38	2

sw:MLEN_HUMAN	P16475	Myosin light chain alkali, non-muscle isoform	39	3
sw:CALX_HUMAN	P27824	Calnexin precursor	40	3
sw:MA32_HUMAN	Q07021	Complement component 1	41	<2
sw:NUAM_HUMAN	P28331	NADH-ubiquinone oxidoreductase 75 kda subunit, mitochondrial precursor	42	2
sw:PBEF_HUMAN	P43490	Pre-B cell enhancing factor precursor.	43	2
sw:RET1_HUMAN	P09455	Retinol-binding protein I, cellular	44	2
sw:TCPG_HUMAN	P49368	T-complex protein 1, gamma subunit	45	2
sw:RINI_HUMAN	P13489	Placental ribonuclease inhibitor	46	<2
sw:GBLP_HUMAN	P25388	Guanine nucleotide-binding protein beta subunit-like protein 12.3	47	2
sw:S109_HUMAN	P06702	Calgranulin B	49	<2

Table 3: Proteins up-regulated in pancreatic cancer II

Protein	Acc No	Description	Seq ID No	Fold Change
sw:CAPG_HUMAN	P40121	Macrophage capping protein	50	3
sw:ANX1_HUMAN	P04083	Annexin I (lipocortin I) (calpactin II)	51	4
sw:K2C7_HUMAN	P08729	Keratin, type II cytoskeletal 7	52	5
humangp:CHR13-Q15063	Q15063	Osteoblast specific factor 2 precursor	53	2
sw:TGLC_HUMAN	P21980	Protein-glutamine gamma-glutamyltransferase	54	2
sw:GDIR_HUMAN	P52565	Rho GDP-dissociation inhibitor 1	55	<2
sw:IQG1_HUMAN	P46940	Ras GTPase-activating-like protein	25	2

Table 4. Proteins roughly classified by their involved biological processing or basic function

Protein function^a	Number^b	Percentage (%)^c
Structural constitutal and regulation of cytoskeleton	61	20.8
Cell cycle and metabolism	74	25.3
Response to external stimulus or stress	61	20.8
Signal transduction	13	4.4
Nuclear function	18	6.1
Transport processing	19	6.5
Hemostatis	12	4.1
Cell adhesion	7	2.4
Chaperon	7	2.4
Apoptosis	3	1
Unknown function	11	3.7
Others	7	2.4
Total	293	100

Table 5. Proteins with higher levels in normal pancreatic compared to cancer tissue

Protein ^a	AccNo ^b	Description ^c	Fold ^d	Seq ID No.
cytoskeletal regulation				
sw:DESM_HUMAN	P17661	desmin.	3	70
proteolysis and peptidolysis				
sw:CBPB_HUMAN	P15086	carboxypeptidase b precursor	2	71
sw:CBP1_HUMAN	P15085	carboxypeptidase a1 precursor	Uncalculated	72
sw:CPB2_HUMAN	P50454	carboxypeptidase a2 precursor	Uncalculated	73
sw:CTRB_HUMAN	P17538	chymotrypsinogen b precursor	Uncalculated	74
sw:TRY1_HUMAN	P07477	trypsin i precursor (ec 3.4.21.4) (cationic trypsinogen).	Uncalculated	75
sw:TRY2_HUMAN	P07478	trypsin ii precursor (anionic trypsinogen).	3	76
sw:ILEU_HUMAN	P30740	leukocyte elastase inhibitor	4	77
chaperon				
sw:CH60_HUMAN	P10809	human. mitochondrial matrix protein p1 precursor	2	78
sw:ENPL_HUMAN	P14625	94 kda glucose-regulated protein	3	79
SW:ER29_HUMAN	P30040	endoplasmic reticulum protein erp29 precursor	2	80
sw:PDA2_HUMAN	Q13087	protein disulfide isomerase a2 precursor	2	81
sw:PDA3_HUMAN	P30101	protein disulfide isomerase a3 precursor	2	82
oxidoreductase				
sw:ADHB_HUMAN	P00325	alcohol dehydrogenase beta chain	<2	83
sw:GTO1_HUMAN	P78417	glutathione transferase omega 1	Uncalculated	84
sw:OXRP_HUMAN	Q9Y4L1	150 kda oxygen-regulated protein precursor	Uncalculated	85

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sw:PDX4_HUMAN	Q13162	peroxiredoxin 4	<2	86
sw:ULA4_HUMAN	P30039	mawd binding protein	<2	87
metabolism of biological process				
sw:AMYC_HUMAN	P19961	alpha-amylase 2b precursor	3	88
sw:AMYP_HUMAN	P04746	alpha-amylase, pancreatic precursor	Uncalculated	89
sw:ATPA_HUMAN	P25705	atp synthase alpha chain, mitochondrial precursor	<2	90
sw:BAL_HUMAN	P19835	bile-salt-activated lipase precursor	3	91
sw:LIP1_HUMAN	P54315	pancreatic lipase related protein 1 precursor	<2	92
sw:LIP2_HUMAN	P54317	pancreatic lipase related protein 2 precursor	Uncalculated	93
sw:LIPP_HUMAN	P16233	triacylglycerol lipase, pancreatic precursor	Uncalculated	94
sw:DPY2_HUMAN	Q16555	dihydropyrimidinase related protein-2		95
sw:GABT_HUMAN	P80404	4-aminobutyrate aminotransferase	2	96
sw:GATM_HUMAN	P50440	glycine amidinotransferase, mitochondrial precursor	Uncalculated	97
sw:GR78_HUMAN	P11021	78 kda glucose-regulated protein precursor (grp 78)	3	98
sw:IF32_HUMAN	Q13347	eukaryotic translation initiation factor 3 subunit 2	<2	99
sw:DPY2_HUMAN	Q16555	dihydropyrimidinase related protein-2		100
sw:PGMU_HUMAN	P36871	phosphoglucomutase	2	101
sw:PSA1_HUMAN	P25786	proteasome subunit alpha type 1	2	102
heat shock protein				
sw:HS27_HUMAN	P04792	heat shock 27 kda protein	Uncalculated	103
signaling				
SW:PD6I	Q8WUM4	programmed cell death 6 interacting protein	5	104
muscle development				

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hsugp:057687-10-0	Q9bva2	four and a half lim domains 3	<2	105
SW:sli2	Q13643	Skeletal muscle LIM-protein 2 (SLIM 2)(Four and a half LIM domains protein 3)(PHL3).	<2	106
transport of biological process				
sw:CYB5_HUMAN	P00167	cytochrome b5.	2	107
cell adhesion				
sw:PAP1_HUMAN	Q06141	pancreatitis-associated protein 1 precursor.	Uncalculated	108
other				
SW:CA16_HUMAN	P12109	collagen alpha 1(vi) chain precursor.	5	109
SW:LUM_HUMAN	P51884	lumican precursor	3	110

Table 6 Proteins with higher levels in pancreatic cancer compared to in normal tissue

Protein ^a	AccNo ^b	Description ^c	Fold ^d	Seq ID No.
cytoskeletal regulation				
sw:FSC2_HUMAN	O14926	fascin 2 (retinal fascin).	2	56
sw:AAC1_HUMAN	P12814	alpha-actinin 1	2	7
sw:AAC4_HUMAN	O43707	alpha-actinin 4	2	5
sw:ABP2_HUMAN	P21333	endothelial actin-binding protein (alpha-filamin).	4	9
sw:ANX2_HUMAN	P07355	human annexin ii (lipocortin ii)	2	19
sw:CALD_HUMAN	Q05682	caldesmon (cdm).	2	12
sw:CAPB_HUMAN	P47756	f-actin capping protein beta subunit	5	15
sw:CAPG_HUMAN	P40121	macrophage capping protein	3	50
sw:COF1_HUMAN	P23528	cofilin, non-muscle isoform (p18).	<2	21
sw:DEST_HUMAN	P18282	destrin (actin-depolymerizing factor) (adf).	2	57
sw:DYI2_HUMAN	Q13409	dynein intermediate chain 2(fragment).	2	23
sw:GELS_HUMAN	P06396	gelsolin precursor	3	3
sw:K1CS_HUMAN	P08727	keratin, type i cytoskeletal 19	4	33
sw:K2C7_HUMAN	P08729	keratin, type ii cytoskeletal 7	5	52
sw:MLEN_HUMAN	P16475	myosin light chain alkali	3	39
sw:PLSL_HUMAN	P13796	l-plastin (lymphocyte cytosolic protein 1)	<2	26
sw:TAGL_HUMAN	P37802	transgelin (22 kda actin-binding protein).	2	10
sw:TBA4_HUMAN	P05215	tubulin alpha-4 chain.	2	8
proteolysis and peptidolysis				
sw:ACY1_HUMAN	Q03154	aminoacylase-1	5	14
sw:AMPL_HUMAN	P28838	cytosol aminopeptidase	3	32
sw:CATD_HUMAN	P07339	cathepsin d precursor.	<2	1

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sw:CFAB_HUMAN	P00751	complement factor b precursor	5	4
sw:EL3A_HUMAN	P09093	elastase iia precursor	4	35
chaperon				
sw:APE_HUMAN	P02649	apolipoprotein e precursor (apo-e).	<2	59
sw:CALX_HUMAN	P27824	calnexin precursor(p90)	3	40
sw:CYPH_HUMAN	P05092	peptidyl-prolyl cis-trans isomerase a	<2	22
sw:TCPG_HUMAN	P49368	t-complex protein 1, gamma subunit	2	45
sw:CBP2_HUMAN	P50454	human. collagen-binding protein 2 precurso	2	20
tr_hum:Q96C61	Q96C61	hypothetical 88.6 kda protein	5	60
oxidoreductase				
sw:DLDH_HUMAN	P09622	dihydrolipoamide dehydrogenase	2	36
sw:IDHC_HUMAN	O75874	isocitrate dehydrogenase [nadp] cytoplasmic	2	2
sw:NUAM_HUMAN	P28331	nadh-ubiquinone oxidoreductase 75 kda subunit	2	42
metabolism of biological process				
sw:ALDX_HUMAN	P14550	alcohol dehydrogenase [nadp+]	4	34
sw:ECH1_HUMAN	Q13011	delta3,5-delta2,4-dienoyl-coa isomerase	2	24
sw:ECHM_HUMAN	P30084	enoyl-coa hydratase, mitochondrial precursor	3	37
sw:IPYR_HUMAN	Q15181	inorganic pyrophosphatase	<2	16
sw:TYPH_HUMAN	P19971	thymidine phosphorylase precursor	5	31
SW:ENOA_HUMAN	P06733	human alpha enolase	2	61
sw:ENOL_HUMAN	Q05524	alpha enolase, lung specific	2	13
sw:SYW_HUMAN	P23381	tryptophanyl-trna synthetase	2	62
heat shock protein				
sw:HSBX_HUMAN	O14558	heat-shock 20 kda like-protein p20.	2	38
signaling				
sw:GBLP_HUMAN	P25388	guanine nucleotide-binding protein beta subunit-like protein 12.3	2	47

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sw:GDIR_HUMAN	P52565	rho gdp-dissociation inhibitor 1	<2	55
sw:IQG1_HUMAN	P46940	ras gtpase-activating-like protein iqgap1	2	25
sw:PBEF_HUMAN	P43490	pre-b cell enhancing factor precursor.	2	43
sw:RAN_HUMAN	P17080	gtp-binding nuclear protein ran	3	27
immune response				
sw:KAC_HUMAN	P01834	ig kappa chain c region.	2	63
sw:MA32_HUMAN	Q07021	pre-mrna splicing factor sf2, p32 subunit.	<2	41
inflammatory reponse				
sw:ANX1_HUMAN	P04083	annexin i (lipocortin i)	4	51
sw:LEG3_HUMAN	P17931	galectin-3	2	17
sw:S109_HUMAN	P06702	calgranulin b (mrp-14)	<2	49
muscle development				
sw:TPM1_HUMAN	P09493	tropomyosin 1 alpha chain	<2	30
sw:TPM4_HUMAN	P07226	tropomyosin alpha 4 chain	<2	11
sw:MLRN_HUMAN	P24844	myosin regulatory light chain 2	2	48
transport of biological process				
humangp:CHR2-Q15092	Q15092	transmembrane protein.	2	64
sw:POR2_HUMAN	P45880	voltage-dependent anion-selective channel protein 2	<2	18
sw:RET1_HUMAN	P09455	retinol-binding protein 1	2	44
RNA processing				
humangp:CHR20-Q9P2E9	O75300	ribosome binding protein 1 (kiaa1398 protein).	<2	65
sw:RINI_HUMAN	P13489	placental ribonuclease inhibitor	<2	46
sw:ROK_HUMAN	Q07244	heterogeneous nuclear ribonucleoprotein k	2	28
blood coagulation				
sw:FIBG_HUMAN	P02679	fibrinogen gamma chain precursor	3	66
sw:THRB_HUMAN	P00734	prothrombin precursor	<2	67
Anti-apoptosis				

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sw:TCTP_HUMAN	P13693	translationally controlled tumor protein (p23)	<2	29
cell adhesion				
humangp:CHR13-Q15063	Q15063	osteoblast specific factor 2 precursor	2	53
sw:BGH3_HUMAN	Q15582	transforming growth factor-beta induced protein	5	6
other				
sw:TGLC_HUMAN	P21980	tissue transglutaminase	2	54
sw:KPY1_HUMAN	P14618	Human pyruvate kinase, cytosolic thyroid hormone-binding protein	3	68
humangp:CHR19-Q96D15	Q96D15	Reticulocalbin 3 precursor.	2	69

Claims

1. A marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3.
- 5 2. The marker of claim 1 wherein the group from which at least one polypeptide is selected consists of the polypeptides listed in table 2.
3. A polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3, for use as a marker or as a component of a marker for diagnosis of pancreatic
10 cancer and/or the susceptibility to pancreatic cancer.
4. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of
 - a) obtaining a biological sample; and
 - 15 b) detecting and/or measuring the increase of a marker of claims 1 or 2.
5. The in vitro method of claim 4, wherein the marker comprises at least two polypeptides.
- 20 6. The in vitro method of claims 4 or 5 wherein said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.
7. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of
 - 25 a) obtaining a biological sample; and
 - b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker of claims 1 or 2.

8. The in vitro method of claim 7, wherein said nucleic acid molecule is RNA or DNA.
9. The in vitro method of claim 8, wherein said DNA is a cDNA.
- 5
10. The in vitro method of any one of claims 7 to 9, wherein the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual.
- 10
11. The in vitro method of any one of claims 4 to 6, wherein the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.
- 15
12. The in vitro method of claim 11, wherein an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.
13. A screening method for identifying and/or obtaining a compound which interacts
- 20 with a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of
- a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and
- 25 b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

14. A screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of
- 5 a) contacting a said polypeptide with a compound identified and/or obtained by the screening method of claim 13 under conditions which allow interaction of said compound with said polypeptide;
 - b) determining the activity of said polypeptide;
 - c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and
 - 10 d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.
15. A screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of
- a) contacting a host which expresses said polypeptide with a compound,
 - b) determining the expression level and/or activity of said polypeptide;
 - c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and
 - 20 d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.
- 25 16. A compound identified and/or obtained by the screening methods of any one of claims 13 to 15.
17. A pharmaceutical composition comprising the compound of claim 16.

18. A method for the preparation of the pharmaceutical composition of claim 17 comprising formulating the compound of claim 16 in a pharmaceutically acceptable carrier or diluent.
- 5 19. Use of a compound of claim 16 for the preparation of a medicament for the treatment or prevention of pancreatic cancer.
20. Use of a compound of claim 16 for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer.
- 10 21. The use of claim 19 or 20 wherein said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.
- 15 22. Antibodies against the proteins listed in tables 2 and/or 3, or antigen-binding fragments thereof, for the use in an in vitro method for the diagnosis of pancreatic cancer.
23. A kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, of claim 22.
- 20 24. A kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker of claims 1 or 2.
- 25 25. A kit for screening of compounds that activate or inhibit any of the polypeptides listed in tables 2 and/or 3, or stimulate or inhibit the expression of any of said polypeptides.

26. A marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6.
27. The marker of claim 26, wherein said at least one polypeptide does not include Seq
5 ID No.s 25 and 50 to 55.
28. The marker according to any one of claims 26 to 27, additionally comprising at least one of the polypeptides listed in table 5.
- 10 29. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of
- a) obtaining a biological sample; and
- b) detecting and/or measuring the increase of at least one of the polypeptides listed in table 6.
- 15
30. The in vitro method of claim 29, additionally comprising the step of detecting and/or measuring the decrease of at least one of the polypeptides listed in table 5.
31. The in vitro method of claims 29 or 30, wherein said at least one polypeptide does
20 not include Seq ID No.s 25 and 50 to 55.
32. The in vitro method of any one of claims 29 to 31, wherein said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.
- 25
33. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

- a) obtaining a biological sample; and
 - b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker of any one of claims 26 to 28.
- 5 34. The in vitro method of claim 33, wherein said nucleic acid molecule is RNA or DNA.
35. The in vitro method of claim 34, wherein said DNA is a cDNA.
- 10 36. The in vitro method of any one of claims 33 to 35, wherein the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual.
- 15 37. The in vitro method of any one of claims 33 to 36, wherein the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.
- 20 38. The in vitro method of claim 37, wherein an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.
39. A screening method for identifying and/or obtaining a compound which interacts with a polypeptide selected from the group consisting of the polypeptides listed in table 6
25 whose expression is upregulated in pancreatic cancer, comprising the steps of
- a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

40. A screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of
- a) contacting said polypeptide with a compound identified and/or obtained by the screening method of claim 39 under conditions which allow interaction of said compound with said polypeptide;
 - 10 b) determining the activity of said polypeptide;
 - c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and
 - d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.
- 15

41. A screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of
- a) contacting a host which expresses said polypeptide with a compound,
 - b) determining the expression level and/or activity of said polypeptide;
 - c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and
 - 25 d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

42. A compound identified and/or obtained by the screening methods of any one of claims 39 to 41.

43. A pharmaceutical composition comprising the compound of claim 42.

5

44. A method for the preparation of the pharmaceutical composition of claim 43 comprising formulating the compound of claim 42 in a pharmaceutically acceptable carrier or diluent.

10 45. Use of a compound of claim 42 for the preparation of a medicament for the treatment or prevention of pancreatic cancer.

46. Use of a compound of claim 42 for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer.

15

47. The use of claim 45 or 46 wherein said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

48. Antibodies against the proteins listed in tables 5 and/or 6, or antigen-binding
20 fragments thereof, for the use in an in vitro method for the diagnosis of pancreatic cancer.

49. A kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, of claim 48.

25

50. A kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker of claims 26 to 28.

51. A kit for screening of compounds that activate or inhibit any of the polypeptides listed in table 5 and/or 6, or stimulate or inhibit the expression of any of said polypeptides.

5

52. The kit of claim 51, wherein said polypeptides are the polypeptides listed in table 6.

53. The proteins, compounds, kits, methods and uses substantially as herein before described, especially with reference to the foregoing examples.

10

SEQUENCE LISTING

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<223> Accession No. as of 06 Dec 2002: P07339

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Lys Gly Pro Val Ser Lys Tyr Ser Gln Ala Val Pro Ala Val Thr Glu
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Gly Pro Ile Pro Glu Val Leu Lys Asn Tyr Met Asp Ala Gln Tyr Tyr
65 70 75 80
5 Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Cys Phe Thr Val Val Phe
85 90 95
Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Ile His Cys Lys Leu
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Leu Asp Ile Ala Cys Trp Ile His His Lys Tyr Asn Ser Asp Lys Ser
10 115 120 125
Ser Thr Tyr Val Lys Asn Gly Thr Ser Phe Asp Ile His Tyr Gly Ser
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Ala Lys Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro Arg Ile Ser Val
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Pro Gly Gly Glu Leu Met Leu Gly Gly Thr Asp Ser Lys Tyr Tyr Lys
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Gly Ser Leu Ser Tyr Leu Asn Val Thr Arg Lys Ala Tyr Trp Gln Val
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5 His Leu Asp Gln Val Glu Val Ala Ser Gly Leu Thr Leu Cys Lys Glu
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Gly Cys Glu Ala Ile Val Asp Thr Gly Thr Ser Leu Met Val Gly Pro
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Val Asp Glu Val Arg Glu Leu Gln Lys Ala Ile Gly Ala Val Pro Leu
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Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu Ala Ile

50 55 60

Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro Asp Glu

20 65 70 75 80

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15 Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln Phe Glu
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Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys Asn Tyr
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Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr Val Glu
290 295 300

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Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe Ala Trp
325 330 335
5 Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys Glu Leu
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10 370 375 380
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Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
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8/335

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225 230 235 240

Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala
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Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln
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Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala
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15 Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser
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Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg
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Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys
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15 Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu
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Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp
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725 730 735

Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu
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11/335

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<223> Accession No. as of 06 Dec 2002: P00751

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10

15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg

20

20

25

30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser

35

40

45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser

50

55

60

12/335

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65 70 75 80
Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
85 90 95
5 Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
100 105 110
Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
115 120 125
Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
10 130 135 140
Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145 150 155 160
Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
165 170 175
15 Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
180 185 190
Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
195 200 205
Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
20 210 215 220
Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225 230 235 240
Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
245 250 255

13/335

Gln Lys Arg Lys Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
260 265 270

Leu Val Leu Asp Gly Ser Asp Ser Ile Gly Ala Ser Asn Phe Thr Gly
275 280 285

5 Ala Lys Lys Cys Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
290 295 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305 310 315 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
10 325 330 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
340 345 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
355 360 365

15 Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
370 375 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385 390 395 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
20 405 410 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
420 425 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
435 440 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
450 455 460
Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465 470 475 480
5 Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
485 490 495
Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
500 505 510
Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
-10 515 520 525
Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
530 535 540
Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545 550 555 560
15 Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
565 570 575
Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
580 585 590
Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
20 595 600 605
Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
610 615 620
Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625 630 635 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
645 650 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
660 665 670

5 Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
675 680 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
690 695 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
10 705 710 715 720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
725 730 735

His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
740 745 750

15 Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu
755 760

<210> 5

20 <211> 911

<212> PRT

<213> Homo sapiens

<220>

<221> Alpha-actinin 4

<222> (1)..(911)

<223> Accession No. 043707

<400> 5

5 Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
1 5 10 15
Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
20 25 30
Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
10 35 40 45
Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu
50 55 60
Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp
65 70 75 80
15 Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu
85 90 95
Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val
100 105 110
Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser
20 115 120 125
Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly
130 135 140
Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val
145 150 155 160

Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys
165 170 175

Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp
180 185 190

5 Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu
195 200 205

Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu
210 215 220

Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met
10 225 230 235 240

Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala
245 250 255

Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln
260 265 270

15 Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn
275 280 285

Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp
290 295 300

Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp Arg Val
20 305 310 315 320

Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg
325 330 335

Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln
340 345 350

Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn
355 360 365

Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp Ile Asn
370 375 380

5 Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp
385 390 395 400

Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu
405 410 415

Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys
10 420 425 430

Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp
435 440 445

Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala
450 455 460

15 Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu
465 470 475 480

Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg Cys Gln
485 490 495

Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His Ser Arg
20 500 505 510

Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln
515 520 525

Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met
530 535 540

Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val His Thr Ile
545 550 555 560
Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr
565 570 575
5 Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys
580 585 590
Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser
595 600 605
Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu
10 610 615 620
Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu
625 630 635 640
Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser
645 650 655
15 Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile
660 665 670
Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser
675 680 685
His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu
20 690 695 700
Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe
705 710 715 720
Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp
725 730 735

Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn
740 745 750

Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln
755 760 765

5 Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly Gly Ala
770 775 780

Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp
785 790 795 800

Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn Arg Ile Met Ser
10 805 810 815

Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe Ile
820 825 830

Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln Val
835 840 845

15 Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala
850 855 860

Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile
865 870 875 880

Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val Pro Gly Ala Leu
20 885 890 895

Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
900 905 910

<210> 6

<211> 683

<212> PRT

<213> Homo sapiens

5 <220>

<221> Transforming growth factor-beta induced protein IG-H3 precursor

<222> (1)..(683)

<223> Accession No. as of 06 Dec 2002: Q15582

<400> 6

10

Met Ala Leu Phe Val Arg Leu Leu Ala Leu Ala Leu Ala Leu Ala Leu

1 5 10 15

Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu

20 25 30

15 Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val

35 40 45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn

50 55 60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile

20 65 70 75 80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly

85 90 95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val

100 105 110

Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
115 120 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
130 135 140

5 Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val
145 150 155 160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
165 170 175

Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
10 180 185 190

Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
195 200 205

Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala
210 215 220

15 Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr
225 230 235 240

Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu
245 250 255

Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn
20 260 265 270

Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile
275 280 285

Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg
290 295 300

23/335

Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala
305 310 315 320
Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu
325 330 335
5 Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile
340 345 350
Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp
355 360 365
Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala
10 370 375 380
Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu
385 390 395 400
Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
405 410 415
15 Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg
420 425 430
Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr
435 440 445
Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg
20 450 455 460
Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala
465 470 475 480
Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg
485 490 495

Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp
500 505 510

Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
515 520 525

5 Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
530 535 540

Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly
545 550 555 560

Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
10 565 570 575

Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
580 585 590

Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val
595 600 605

15 Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
610 615 620

Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln
625 630 635 640

Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln
20 645 650 655

Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro
660 665 670

Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His
675 680

<210> 7

<211> 892

5 <212> PRT

<213> Homo sapiens

<220>

<221> Alpha-actinin 1

<222> (1)..(892)

10 <223> Accession No. P12814

<400> 7

Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu

1 5 10 15

15 Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln

20 25 30

Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala

35 40 45

Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys

20 50 55 60

Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro

65 70 75 80

Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala

85 90 95

26/335

Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala
100 105 110

Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp
115 120 125

5 Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr
130 135 140

Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro
145 150 155 160

Tyr Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly
10 165 170 175

Leu Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp
180 185 190

Tyr Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala
195 200 205

15 Phe Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala
210 215 220

Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr
225 230 235 240

Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu
20 245 250 255

Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn
260 265 270

Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu
275 280 285

Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu Asn
290 295 300
Thr Met His Ala Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg
305 310 315 320
5 Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile
325 330 335
Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala
340 345 350
Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp
10 355 360 365
Gly Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn
370 375 380
Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg
385 390 395 400
15 Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met
405 410 415
Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala
420 425 430
Leu Leu Lys Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln
20 435 440 445
Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu
450 455 460
Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys
465 470 475 480

Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala
485 490 495

Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu
500 505 510

5 Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala
515 520 525

Met Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile
530 535 540

Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp
10 545 550 555 560

Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser
565 570 575

Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr
580 585 590

15 Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg
595 600 605

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg
610 615 620

Gln Gln His Asn Glu Ser Val Arg Lys Gln Phe Gly Ala Gln Ala Asn
20 625 630 635 640

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile
645 650 655

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg
660 665 670

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu
675 680 685

Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys
690 695 700

5 His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu
705 710 715 720

Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu
725 730 735

Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg
10 740 745 750

Ala Ser Phe Asn His Phe Asp Arg Asp His Ser Gly Thr Leu Gly Pro
755 760 765

Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Ile Gly Asn
770 775 780

15 Asp Pro Gln Gly Glu Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp
785 790 795 800

Pro Asn Arg Leu Gly Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met
805 810 815

Ser Arg Glu Thr Ala Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser
20 820 825 830

Phe Lys Ile Leu Ala Gly Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu
835 840 845

Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met
850 855 860

30/335

Ala Pro Tyr Thr Gly Pro Asp Ser Val Pro Gly Ala Leu Asp Tyr Met

865

870

875

880

Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu

885

890

5

<210> 8

<211> 448

<212> PRT

10 <213> Homo sapiens

<220>

<221> Tubulin alpha-4 chain

<222> (1)..(448)

<223> Accession No. P05215

15 <400> 8

Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln Met

1

5

10

15

Gly Asn Ala Cys Trp Glu Leu Tyr Cys Leu Glu His Gly Ile Gln Pro

20

20

25

30

Asp Gly Gln Met Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp Asp Ser

35

40

45

Phe Thr Thr Phe Phe Cys Glu Thr Gly Ala Gly Lys His Val Pro Arg

50

55

60

Ala Val Phe Val Asp Leu Glu Pro Thr Val Ile Asp Glu Ile Arg Asn
65 70 75 80
Gly Pro Tyr Arg Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly Lys
85 90 95
5 Glu Asp Ala Ala Asn Asn Tyr Ala Arg Gly His Tyr Thr Ile Gly Lys
100 105 110
Glu Ile Ile Asp Pro Val Leu Asp Arg Ile Arg Lys Leu Ser Asp Gln
115 120 125
Cys Thr Gly Leu Gln Gly Phe Leu Val Phe His Ser Phe Gly Gly Gly
10 130 135 140
Thr Gly Ser Gly Phe Thr Ser Leu Leu Met Glu Arg Leu Ser Val Asp
145 150 155 160
Tyr Gly Lys Lys Ser Lys Leu Glu Phe Ser Ile Tyr Pro Ala Pro Gln
165 170 175
15 Val Ser Thr Ala Val Val Glu Pro Tyr Asn Ser Ile Leu Thr Thr His
180 185 190
Thr Thr Leu Glu His Ser Asp Cys Ala Phe Met Val Asp Asn Glu Ala
195 200 205
Ile Tyr Asp Ile Cys Arg Arg Asn Leu Asp Ile Glu Arg Pro Thr Tyr
20 210 215 220
Thr Asn Leu Asn Arg Leu Ile Ser Gln Ile Val Ser Ser Ile Thr Ala
225 230 235 240
Ser Leu Arg Phe Asp Gly Ala Leu Asn Val Asp Leu Thr Glu Phe Gln
245 250 255

32/335

Thr Asn Leu Val Pro Tyr Pro Arg Ile His Phe Pro Leu Ala Thr Tyr
260 265 270

Ala Pro Val Ile Ser Ala Glu Lys Ala Tyr His Glu Gln Leu Ser Val
275 280 285

5 Ala Glu Ile Thr Asn Ala Cys Phe Glu Pro Ala Asn Gln Met Val Lys
290 295 300

Cys Asp Pro Arg His Gly Lys Tyr Met Ala Cys Cys Leu Leu Tyr Arg
305 310 315 320

Gly Asp Val Val Pro Lys Asp Val Asn Ala Ala Ile Ala Ala Ile Lys
10 325 330 335

Thr Lys Arg Ser Ile Gln Phe Val Asp Trp Cys Pro Thr Gly Phe Lys
340 345 350

Val Gly Ile Asn Tyr Gln Pro Pro Thr Val Val Pro Gly Gly Asp Leu
355 360 365

15 Ala Lys Val Gln Arg Ala Val Cys Met Leu Ser Asn Thr Thr Ala Ile
370 375 380

Ala Glu Ala Trp Ala Arg Leu Asp His Lys Phe Asp Leu Met Tyr Ala
385 390 395 400

Lys Arg Ala Phe Val His Trp Tyr Val Gly Glu Gly Met Glu Glu Gly
20 405 410 415

Glu Phe Ser Glu Ala Arg Glu Asp Met Ala Ala Leu Glu Lys Asp Tyr
420 425 430

Glu Glu Val Gly Ile Asp Ser Tyr Glu Asp Glu Asp Glu Gly Glu Glu
435 440 445

<210> 9
<211> 2647
5 <212> PRT
<213> Homo sapiens
<220>
<221> Filamin A
<222> (1)..(2647)
10 <223> Accession No. P21333
<400> 9

Met Ser Ser Ser His Ser Arg Ala Gly Gln Ser Ala Ala Gly Ala Ala
1 5 10 15
15 Pro Gly Gly Gly Val Asp Thr Arg Asp Ala Glu Met Pro Ala Thr Glu
20 25 30
Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln Asn Thr
35 40 45
Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Ser Lys Arg Ile
20 50 55 60
Ala Asn Leu Gln Thr Asp Leu Ser Asp Gly Leu Arg Leu Ile Ala Leu
65 70 75 80
Leu Glu Val Leu Ser Gln Lys Lys Met His Arg Lys His Asn Gln Arg
85 90 95

Pro Thr Phe Arg Gln Met Gln Leu Glu Asn Val Ser Val Ala Leu Glu
100 105 110

Phe Leu Asp Arg Glu Ser Ile Lys Leu Val Ser Ile Asp Ser Lys Ala
115 120 125

5 Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly Leu Ile Trp Thr Leu
130 135 140

Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp Asp Glu Glu Glu Asp
145 150 155 160

Glu Glu Ala Lys Lys Gln Thr Pro Lys Gln Arg Leu Leu Gly Trp Ile
10 165 170 175

Gln Asn Lys Leu Pro Gln Leu Pro Ile Thr Asn Phe Ser Arg Asp Trp
180 185 190

Gln Ser Gly Arg Ala Leu Gly Ala Leu Val Asp Ser Cys Ala Pro Gly
195 200 205

15 Leu Cys Pro Asp Trp Asp Ser Trp Asp Ala Ser Lys Pro Val Thr Asn
210 215 220

Ala Arg Glu Ala Met Gln Gln Ala Asp Asp Trp Leu Gly Ile Pro Gln
225 230 235 240

Val Ile Thr Pro Glu Glu Ile Val Asp Pro Asn Val Asp Glu His Ser
20 245 250 255

Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys Pro Gly
260 265 270

Ala Pro Leu Arg Pro Lys Leu Asn Pro Lys Lys Ala Arg Ala Tyr Gly
275 280 285

35/335

Pro Gly Ile Glu Pro Thr Gly Asn Met Val Lys Lys Arg Ala Glu Phe
290 295 300

Thr Val Glu Thr Arg Ser Ala Gly Gln Gly Glu Val Leu Val Tyr Val
305 310 315 320

5 Glu Asp Pro Ala Gly His Gln Glu Glu Ala Lys Val Thr Ala Asn Asn
325 330 335

Asp Lys Asn Arg Thr Phe Ser Val Trp Tyr Val Pro Glu Val Thr Gly
340 345 350

Thr His Lys Val Thr Val Leu Phe Ala Gly Gln His Ile Ala Lys Ser
10 355 360 365

Pro Phe Glu Val Tyr Val Asp Lys Ser Gln Gly Asp Ala Ser Lys Val
370 375 380

Thr Ala Gln Gly Pro Gly Leu Glu Pro Ser Gly Asn Ile Ala Asn Lys
385 390 395 400

15 Thr Thr Tyr Phe Glu Ile Phe Thr Ala Gly Ala Gly Thr Gly Glu Val
405 410 415

Glu Val Val Ile Gln Asp Pro Met Gly Gln Lys Gly Thr Val Glu Pro
420 425 430

Gln Leu Glu Ala Arg Gly Asp Ser Thr Tyr Arg Cys Ser Tyr Gln Pro
20 435 440 445

Thr Met Glu Gly Val His Thr Val His Val Thr Phe Ala Gly Val Pro
450 455 460

Ile Pro Arg Ser Pro Tyr Thr Val Thr Val Gly Gln Ala Cys Asn Pro
465 470 475 480

Ser Ala Cys Arg Ala Val Gly Arg Gly Leu Gln Pro Lys Gly Val Arg
485 490 495

Val Lys Glu Thr Ala Asp Phe Lys Val Tyr Thr Lys Gly Ala Gly Ser
500 505 510

5 Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Glu Glu Arg Val
515 520 525

Lys Gln Lys Asp Leu Gly Asp Gly Val Tyr Gly Phe Glu Tyr Tyr Pro
530 535 540

Met Val Pro Gly Thr Tyr Ile Val Thr Ile Thr Trp Gly Gly Gln Asn
10 545 550 555 560

Ile Gly Arg Ser Pro Phe Glu Val Lys Val Gly Thr Glu Cys Gly Asn
565 570 575

Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Gly Gly Val Val Gly
580 585 590

15 Lys Ser Ala Asp Phe Val Val Glu Ala Ile Gly Asp Asp Val Gly Thr
595 600 605

Leu Gly Phe Ser Val Glu Gly Pro Ser Gln Ala Lys Ile Glu Cys Asp
610 615 620

Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp Pro Gln Glu Ala
20 625 630 635 640

Gly Glu Tyr Ala Val His Val Leu Cys Asn Ser Glu Asp Ile Arg Leu
645 650 655

Ser Pro Phe Met Ala Asp Ile Arg Asp Ala Pro Gln Asp Phe His Pro
660 665 670

Asp Arg Val Lys Ala Arg Gly Pro Gly Leu Glu Lys Thr Gly Val Ala
675 680 685

Val Asn Lys Pro Ala Glu Phe Thr Val Asp Ala Lys His Gly Gly Lys
690 695 700

5 Ala Pro Leu Arg Val Gln Val Gln Asp Asn Glu Gly Cys Pro Val Glu
705 710 715 720

Ala Leu Val Lys Asp Asn Gly Asn Gly Thr Tyr Ser Cys Ser Tyr Val
725 730 735

Pro Arg Lys Pro Val Lys His Thr Ala Met Val Ser Trp Gly Gly Val
10 740 745 750

Ser Ile Pro Asn Ser Pro Phe Arg Val Asn Val Gly Ala Gly Ser His
755 760 765

Pro Asn Lys Val Lys Val Tyr Gly Pro Gly Val Ala Lys Thr Gly Leu
770 775 780

15 Lys Ala His Glu Pro Thr Tyr Phe Thr Val Asp Cys Ala Glu Ala Gly
785 790 795 800

Gln Gly Asp Val Ser Ile Gly Ile Lys Cys Ala Pro Gly Val Val Gly
805 810 815

Pro Ala Glu Ala Asp Ile Asp Phe Asp Ile Ile Arg Asn Asp Asn Asp
20 820 825 830

Thr Phe Thr Val Lys Tyr Thr Pro Arg Gly Ala Gly Ser Tyr Thr Ile
835 840 845

Met Val Leu Phe Ala Asp Gln Ala Thr Pro Thr Ser Pro Ile Arg Val
850 855 860

Lys Val Glu Pro Ser His Asp Ala Ser Lys Val Lys Ala Glu Gly Pro
865 870 875 880
Gly Leu Ser Arg Thr Gly Val Glu Leu Gly Lys Pro Thr His Phe Thr
885 890 895
5 Val Asn Ala Lys Ala Ala Gly Lys Gly Lys Leu Asp Val Gln Phe Ser
900 905 910
Gly Leu Thr Lys Gly Asp Ala Val Arg Asp Val Asp Ile Ile Asp His
915 920 925
His Asp Asn Thr Tyr Thr Val Lys Tyr Thr Pro Val Gln Gln Gly Pro
10 930 935 940
Val Gly Val Asn Val Thr Tyr Gly Gly Asp Pro Ile Pro Lys Ser Pro
945 950 955 960
Phe Ser Val Ala Val Ser Pro Ser Leu Asp Leu Ser Lys Ile Lys Val
965 970 975
15 Ser Gly Leu Gly Glu Lys Val Asp Val Gly Lys Asp Gln Glu Phe Thr
980 985 990
Val Lys Ser Lys Gly Ala Gly Gly Gln Gly Lys Val Ala Ser Lys Ile
995 1000 1005
Val Gly Pro Ser Gly Ala Ala Val Pro Cys Lys Val Glu Pro Gly
20 1010 1015 1020
Leu Gly Ala Asp Asn Ser Val Val Arg Phe Leu Pro Arg Glu Glu
1025 1030 1035
Gly Pro Tyr Glu Val Glu Val Thr Tyr Asp Gly Val Pro Val Pro
1040 1045 1050

	Gly Ser	Pro Phe Pro Leu Glu	Ala Val Ala Pro Thr	Lys Pro Ser
	1055		1060	1065
	Lys Val	Lys Ala Phe Gly Pro	Gly Leu Gln Gly Gly	Ser Ala Gly
	1070		1075	1080
5	Ser Pro	Ala Arg Phe Thr Ile	Asp Thr Lys Gly Ala	Gly Thr Gly
	1085		1090	1095
	Gly Leu	Gly Leu Thr Val Glu	Gly Pro Cys Glu Ala	Gln Leu Glu
	1100		1105	1110
	Cys Leu	Asp Asn Gly Asp Gly	Thr Cys Ser Val Ser	Tyr Val Pro
10	1115		1120	1125
	Thr Glu	Pro Gly Asp Tyr Asn	Ile Asn Ile Leu Phe	Ala Asp Thr
	1130		1135	1140
	His Ile	Pro Gly Ser Pro Phe	Lys Ala His Val Val	Pro Cys Phe
	1145		1150	1155
15	Asp Ala	Ser Lys Val Lys Cys	Ser Gly Pro Gly Leu	Glu Arg Ala
	1160		1165	1170
	Thr Ala	Gly Glu Val Gly Gln	Phe Gln Val Asp Cys	Ser Ser Ala
	1175		1180	1185
	Gly Ser	Ala Glu Leu Thr Ile	Glu Ile Cys Ser Glu	Ala Gly Leu
20	1190		1195	1200
	Pro Ala	Glu Val Tyr Ile Gln	Asp His Gly Asp Gly	Thr His Thr
	1205		1210	1215
	Ile Thr	Tyr Ile Pro Leu Cys	Pro Gly Ala Tyr Thr	Val Thr Ile
	1220		1225	1230

	Lys Tyr	Gly Gly Gln Pro Val	Pro Asn Phe Pro Ser	Lys Leu Gln
	1235	1240	1245	
	Val Glu	Pro Ala Val Asp Thr	Ser Gly Val Gln Cys	Tyr Gly Pro
	1250	1255	1260	
5	Gly Ile	Glu Gly Gln Gly Val	Phe Arg Glu Ala Thr	Thr Glu Phe
	1265	1270	1275	
	Ser Val	Asp Ala Arg Ala Leu	Thr Gln Thr Gly Gly	Pro His Val
	1280	1285	1290	
	Lys Ala	Arg Val Ala Asn Pro	Ser Gly Asn Leu Thr	Glu Thr Tyr
10	1295	1300	1305	
	Val Gln	Asp Arg Gly Asp Gly	Met Tyr Lys Val Glu	Tyr Thr Pro
	1310	1315	1320	
	Tyr Glu	Glu Gly Leu His Ser	Val Asp Val Thr Tyr	Asp Gly Ser
	1325	1330	1335	
15	Pro Val	Pro Ser Ser Pro Phe	Gln Val Pro Val Thr	Glu Gly Cys
	1340	1345	1350	
	Asp Pro	Ser Arg Val Arg Val	His Gly Pro Gly Ile	Gln Ser Gly
	1355	1360	1365	
	Thr Thr	Asn Lys Pro Asn Lys	Phe Thr Val Glu Thr	Arg Gly Ala
20	1370	1375	1380	
	Gly Thr	Gly Gly Leu Gly Leu	Ala Val Glu Gly Pro	Ser Glu Ala
	1385	1390	1395	
	Lys Met	Ser Cys Met Asp Asn	Lys Asp Gly Ser Cys	Ser Val Glu
	1400	1405	1410	

	Tyr Ile	Pro Tyr Glu Ala Gly	Thr Tyr Ser Leu Asn	Val Thr Tyr
	1415		1420	1425
	Gly Gly	His Gln Val Pro Gly	Ser Pro Phe Lys Val	Pro Val His
	1430		1435	1440
5	Asp Val	Thr Asp Ala Ser Lys	Val Lys Cys Ser Gly	Pro Gly Leu
	1445		1450	1455
	Ser Pro	Gly Met Val Arg Ala	Asn Leu Pro Gln Ser	Phe Gln Val
	1460		1465	1470
	Asp Thr	Ser Lys Ala Gly Val	Ala Pro Leu Gln Val	Lys Val Gln
10	1475		1480	1485
	Gly Pro	Lys Gly Leu Val Glu	Pro Val Asp Val Val	Asp Asn Ala
	1490		1495	1500
	Asp Gly	Thr Gln Thr Val Asn	Tyr Val Pro Ser Arg	Glu Gly Pro
	1505		1510	1515
15	Tyr Ser	Ile Ser Val Leu Tyr	Gly Asp Glu Glu Val	Pro Arg Ser
	1520		1525	1530
	Pro Phe	Lys Val Lys Val Leu	Pro Thr His Asp Ala	Ser Lys Val
	1535		1540	1545
	Lys Ala	Ser Gly Pro Gly Leu	Asn Thr Thr Gly Val	Pro Ala Ser
20	1550		1555	1560
	Leu Pro	Val Glu Phe Thr Ile	Asp Ala Lys Asp Ala	Gly Glu Gly
	1565		1570	1575
	Leu Leu	Ala Val Gln Ile Thr	Asp Pro Glu Gly Lys	Pro Lys Lys
	1580		1585	1590

	Thr His	Ile Gln Asp Asn His	Asp Gly Thr Tyr Thr	Val Ala Tyr
	1595	1600	1605	
5	Val Pro	Asp Val Thr Gly Arg	Tyr Thr Ile Leu Ile	Lys Tyr Gly
	1610	1615	1620	
	Gly Asp	Glu Ile Pro Phe Ser	Pro Tyr Arg Val Arg	Ala Val Pro
	1625	1630	1635	
	Thr Gly	Asp Ala Ser Lys Cys	Thr Val Thr Val Ser	Ile Gly Gly
10	1640	1645	1650	
	His Gly	Leu Gly Ala Gly Ile	Gly Pro Thr Ile Gln	Ile Gly Glu
	1655	1660	1665	
	Glu Thr	Val Ile Thr Val Asp	Thr Lys Ala Ala Gly	Lys Gly Lys
	1670	1675	1680	
15	Val Thr	Cys Thr Val Cys Thr	Pro Asp Gly Ser Glu	Val Asp Val
	1685	1690	1695	
	Asp Val	Val Glu Asn Glu Asp	Gly Thr Phe Asp Ile	Phe Tyr Thr
	1700	1705	1710	
	Ala Pro	Gln Pro Gly Lys Tyr	Val Ile Cys Val Arg	Phe Gly Gly
20	1715	1720	1725	
	Glu His	Val Pro Asn Ser Pro	Phe Gln Val Thr Ala	Leu Ala Gly
	1730	1735	1740	
	Asp Gln	Pro Ser Val Gln Pro	Pro Leu Arg Ser Gln	Gln Leu Ala
	1745	1750	1755	

	Pro	Gln	Tyr	Thr	Tyr	Ala	Gln	Gly	Gly	Gln	Gln	Thr	Trp	Ala	Pro
	1760						1765					1770			
	Glu	Arg	Pro	Leu	Val	Gly	Val	Asn	Gly	Leu	Asp	Val	Thr	Ser	Leu
	1775						1780					1785			
5	Arg	Pro	Phe	Asp	Leu	Val	Ile	Pro	Phe	Thr	Ile	Lys	Lys	Gly	Glu
	1790						1795					1800			
	Ile	Thr	Gly	Glu	Val	Arg	Met	Pro	Ser	Gly	Lys	Val	Ala	Gln	Pro
	1805						1810					1815			
	Thr	Ile	Thr	Asp	Asn	Lys	Asp	Gly	Thr	Val	Thr	Val	Arg	Tyr	Ala
10	1820						1825					1830			
	Pro	Ser	Glu	Ala	Gly	Leu	His	Glu	Met	Asp	Ile	Arg	Tyr	Asp	Asn
	1835						1840					1845			
	Met	His	Ile	Pro	Gly	Ser	Pro	Leu	Gln	Phe	Tyr	Val	Asp	Tyr	Val
	1850						1855					1860			
15	Asn	Cys	Gly	His	Val	Thr	Ala	Tyr	Gly	Pro	Gly	Leu	Thr	His	Gly
	1865						1870					1875			
	Val	Val	Asn	Lys	Pro	Ala	Thr	Phe	Thr	Val	Asn	Thr	Lys	Asp	Ala
	1880						1885					1890			
	Gly	Glu	Gly	Gly	Leu	Ser	Leu	Ala	Ile	Glu	Gly	Pro	Ser	Lys	Ala
20	1895						1900					1905			
	Glu	Ile	Ser	Cys	Thr	Asp	Asn	Gln	Asp	Gly	Thr	Cys	Ser	Val	Ser
	1910						1915					1920			
	Tyr	Leu	Pro	Val	Leu	Pro	Gly	Asp	Tyr	Ser	Ile	Leu	Val	Lys	Tyr
	1925						1930					1935			

	Asn	Glu	Gln	His	Val	Pro	Gly	Ser	Pro	Phe	Thr	Ala	Arg	Val	Thr
	1940						1945						1950		
	Gly	Asp	Asp	Ser	Met	Arg	Met	Ser	His	Leu	Lys	Val	Gly	Ser	Ala
	1955						1960						1965		
5	Ala	Asp	Ile	Pro	Ile	Asn	Ile	Ser	Glu	Thr	Asp	Leu	Ser	Leu	Leu
	1970						1975						1980		
	Thr	Ala	Thr	Val	Val	Pro	Pro	Ser	Gly	Arg	Glu	Glu	Pro	Cys	Leu
	1985						1990						1995		
	Leu	Lys	Arg	Leu	Arg	Asn	Gly	His	Val	Gly	Ile	Ser	Phe	Val	Pro
10	2000						2005						2010		
	Lys	Glu	Thr	Gly	Glu	His	Leu	Val	His	Val	Lys	Lys	Asn	Gly	Gln
	2015						2020						2025		
	His	Val	Ala	Ser	Ser	Pro	Ile	Pro	Val	Val	Ile	Ser	Gln	Ser	Glu
	2030						2035						2040		
15	Ile	Gly	Asp	Ala	Ser	Arg	Val	Arg	Val	Ser	Gly	Gln	Gly	Leu	His
	2045						2050						2055		
	Glu	Gly	His	Thr	Phe	Glu	Pro	Ala	Glu	Phe	Ile	Ile	Asp	Thr	Arg
	2060						2065						2070		
	Asp	Ala	Gly	Tyr	Gly	Gly	Leu	Ser	Leu	Ser	Ile	Glu	Gly	Pro	Ser
20	2075						2080						2085		
	Lys	Val	Asp	Ile	Asn	Thr	Glu	Asp	Leu	Glu	Asp	Gly	Thr	Cys	Arg
	2090						2095						2100		
	Val	Thr	Tyr	Cys	Pro	Thr	Glu	Pro	Gly	Asn	Tyr	Ile	Ile	Asn	Ile
	2105						2110						2115		

	Lys Phe	Ala Asp Gln His Val	Pro Gly Ser Pro Phe	Ser Val Lys
	2120	2125	2130	
	Val Thr	Gly Glu Gly Arg Val	Lys Glu Ser Ile Thr	Arg Arg Arg
	2135	2140	2145	
5	Arg Ala	Pro Ser Val Ala Asn	Val Gly Ser His Cys	Asp Leu Ser
	2150	2155	2160	
	Leu Lys	Ile Pro Glu Ile Ser	Ile Gln Asp Met Thr	Ala Gln Val
	2165	2170	2175	
	Thr Ser	Pro Ser Gly Lys Thr	His Glu Ala Glu Ile	Val Glu Gly
10	2180	2185	2190	
	Glu Asn	His Thr Tyr Cys Ile	Arg Phe Val Pro Ala	Glu Met Gly
	2195	2200	2205	
	Thr His	Thr Val Ser Val Lys	Tyr Lys Gly Gln His	Val Pro Gly
	2210	2215	2220	
15	Ser Pro	Phe Gln Phe Thr Val	Gly Pro Leu Gly Glu	Gly Gly Ala
	2225	2230	2235	
	His Lys	Val Arg Ala Gly Gly	Pro Gly Leu Glu Arg	Ala Glu Ala
	2240	2245	2250	
	Gly Val	Pro Ala Glu Phe Ser	Ile Trp Thr Arg Glu	Ala Gly Ala
20	2255	2260	2265	
	Gly Gly	Leu Ala Ile Ala Val	Glu Gly Pro Ser Lys	Ala Glu Ile
	2270	2275	2280	
	Ser Phe	Glu Asp Arg Lys Asp	Gly Ser Cys Gly Val	Ala Tyr Val
	2285	2290	2295	

	Val Gln	Glu Pro Gly Asp Tyr	Glu Val Ser Val Lys	Phe Asn Glu
	2300	2305	2310	
	Glu His	Ile Pro Asp Ser Pro	Phe Val Val Pro Val	Ala Ser Pro
	2315	2320	2325	
5	Ser Gly	Asp Ala Arg Arg Leu	Thr Val Ser Ser Leu	Gln Glu Ser
	2330	2335	2340	
	Gly Leu	Lys Val Asn Gln Pro	Ala Ser Phe Ala Val	Ser Leu Asn
	2345	2350	2355	
	Gly Ala	Lys Gly Ala Ile Asp	Ala Lys Val His Ser	Pro Ser Gly
10	2360	2365	2370	
	Ala Leu	Glu Glu Cys Tyr Val	Thr Glu Ile Asp Gln	Asp Lys Tyr
	2375	2380	2385	
	Ala Val	Arg Phe Ile Pro Arg	Glu Asn Gly Val Tyr	Leu Ile Asp
	2390	2395	2400	
15	Val Lys	Phe Asn Gly Thr His	Ile Pro Gly Ser Pro	Phe Lys Ile
	2405	2410	2415	
	Arg Val	Gly Glu Pro Gly His	Gly Gly Asp Pro Gly	Leu Val Ser
	2420	2425	2430	
	Ala Tyr	Gly Ala Gly Leu Glu	Gly Gly Val Thr Gly	Asn Pro Ala
20	2435	2440	2445	
	Glu Phe	Val Val Asn Thr Ser	Asn Ala Gly Ala Gly	Ala Leu Ser
	2450	2455	2460	
	Val Thr	Ile Asp Gly Pro Ser	Lys Val Lys Met Asp	Cys Gln Glu
	2465	2470	2475	

[illegible]

<210> 10

<211> 199

5 <212> PRT

<213> Homo sapiens

<220>

<221> Transgelin 2

<222> (1)..(199)

10 <223> Accession No. as of 06 Dec 2002: P37802

<400> 10

Met Ala Asn Arg Gly Pro Ala Tyr Gly Leu Ser Arg Glu Val Gln Gln
1 5 10 15
15 Lys Ile Glu Lys Gln Tyr Asp Ala Asp Leu Glu Gln Ile Leu Ile Gln
20 25 30
Trp Ile Thr Thr Gln Cys Arg Lys Asp Val Gly Arg Pro Gln Pro Gly
35 40 45
Arg Glu Asn Phe Gln Asn Trp Leu Lys Asp Gly Thr Val Leu Cys Glu
20 50 55 60
Leu Ile Asn Ala Leu Tyr Pro Glu Gly Gln Ala Pro Val Lys Lys Ile
65 70 75 80
Gln Ala Ser Thr Met Ala Phe Lys Gln Met Glu Gln Ile Ser Gln Phe
85 90 95

Leu Gln Ala Ala Glu Arg Tyr Gly Ile Asn Thr Thr Asp Ile Phe Gln

100

105

110

Thr Val Asp Leu Trp Glu Gly Lys Asn Met Ala Cys Val Gln Arg Thr

115

120

125

5 Leu Met Asn Leu Gly Gly Leu Ala Val Ala Arg Asp Asp Gly Leu Phe

130

135

140

Ser Gly Asp Pro Asn Trp Phe Pro Lys Lys Ser Lys Glu Asn Pro Arg

145

150

155

160

Asn Phe Ser Asp Asn Gln Leu Gln Glu Gly Lys Asn Val Ile Gly Leu

10

165

170

175

Gln Met Gly Thr Asn Arg Gly Ala Ser Gln Ala Gly Met Thr Gly Tyr

180

185

190

Gly Met Pro Arg Gln Ile Leu

195

15

<210> 11

<211> 248

<212> PRT

20 <213> Homo sapiens

<220>

<221> Tropomyosin alpha 4 chain

<222> (1)..(248)

<223> Accession No. P07226

<400> 11

Met Ala Gly Leu Asn Ser Leu Glu Ala Val Lys Arg Lys Ile Gln Ala
1 5 10 15
5 Leu Gln Gln Gln Ala Asp Glu Ala Glu Asp Arg Ala Gln Gly Leu Gln
20 25 30
Arg Glu Leu Asp Gly Glu Arg Glu Arg Arg Glu Lys Ala Glu Gly Asp
35 40 45
Val Ala Ala Leu Asn Arg Arg Ile Gln Leu Val Glu Glu Glu Leu Asp
10 50 55 60
Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys Leu Glu Glu Ala
65 70 75 80
Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys Val Ile Glu Asn
85 90 95
15 Arg Ala Met Lys Asp Glu Glu Lys Met Glu Ile Gln Glu Met Gln Leu
100 105 110
Lys Glu Ala Lys His Ile Ala Glu Glu Ala Asp Arg Lys Tyr Glu Glu
115 120 125
Val Ala Arg Lys Leu Val Ile Leu Glu Gly Glu Leu Glu Arg Ala Glu
20 130 135 140
Glu Arg Ala Glu Val Ser Glu Leu Lys Cys Gly Asp Leu Glu Glu Glu
145 150 155 160
Leu Lys Asn Val Thr Asn Asn Leu Lys Ser Leu Glu Ala Ala Ser Glu
165 170 175

51/335

Lys Tyr Ser Glu Lys Glu Asp Lys Tyr Glu Glu Glu Ile Lys Leu Leu

180

185

190

Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu Phe Ala Glu Arg

195

200

205

5 Thr Val Ala Lys Leu Glu Lys Thr Ile Asp Asp Leu Glu Glu Lys Leu

210

215

220

Ala Gln Ala Lys Glu Glu Asn Val Gly Leu His Gln Thr Leu Asp Gln

225

230

235

240

Thr Leu Asn Glu Leu Asn Cys Ile

10

245

<210> 12

<211> 793

15 <212> PRT

<213> Homo sapiens

<220>

<221> Caldesmon

<222> (1)..(793)

20 <223> Accession No. as of 06 Dec 2002: Q05682

<400> 12

Met Asp Asp Phe Glu Arg Arg Arg Glu Leu Arg Arg Gln Lys Arg Glu

1

5

10

15

52/335

Glu Met Arg Leu Glu Ala Glu Arg Ile Ala Tyr Gln Arg Asn Asp Asp
20 25 30

Asp Glu Glu Glu Ala Ala Arg Glu Arg Arg Arg Arg Ala Arg Gln Glu
35 40 45

5 Arg Leu Arg Gln Lys Gln Glu Glu Glu Ser Leu Gly Gln Val Thr Asp
50 55 60

Gln Val Glu Val Asn Ala Gln Asn Ser Val Pro Asp Glu Glu Ala Lys
65 70 75 80

Thr Thr Thr Thr Asn Thr Gln Val Glu Gly Asp Asp Glu Ala Ala Phe
10 85 90 95

Leu Glu Arg Leu Ala Arg Arg Glu Glu Arg Arg Gln Lys Arg Leu Gln
100 105 110

Glu Ala Leu Glu Arg Gln Lys Glu Phe Asp Pro Thr Ile Thr Asp Ala
115 120 125

15 Ser Leu Ser Leu Pro Ser Arg Arg Met Gln Asn Asp Thr Ala Glu Asn
130 135 140

Glu Thr Thr Glu Lys Glu Glu Lys Ser Glu Ser Arg Gln Glu Arg Tyr
145 150 155 160

Glu Ile Glu Glu Thr Glu Thr Val Thr Lys Ser Tyr Gln Lys Asn Asp
20 165 170 175

Trp Arg Asp Ala Glu Glu Asn Lys Lys Glu Asp Lys Glu Lys Glu Glu
180 185 190

Glu Glu Glu Glu Lys Pro Lys Arg Gly Ser Ile Gly Glu Asn Gln Val
195 200 205

53/335

Glu Val Met Val Glu Glu Lys Thr Thr Glu Ser Gln Glu Glu Thr Val
210 215 220

Val Met Ser Leu Lys Asn Gly Gln Ile Ser Ser Glu Glu Pro Lys Gln
225 230 235 240

5 Glu Glu Glu Arg Glu Gln Gly Ser Asp Glu Ile Ser His His Glu Lys
245 250 255

Met Glu Glu Glu Asp Lys Glu Arg Ala Glu Ala Glu Arg Ala Arg Leu
260 265 270

Glu Ala Glu Glu Arg Glu Arg Ile Lys Ala Glu Gln Asp Lys Lys Ile
10 275 280 285

Ala Asp Glu Arg Ala Arg Ile Glu Ala Glu Glu Lys Ala Ala Ala Gln
290 295 300

Glu Arg Glu Arg Arg Glu Ala Glu Glu Arg Glu Arg Met Arg Glu Glu
305 310 315 320

15 Glu Lys Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys
325 330 335

Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala
340 345 350

Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala Ala Glu
20 355 360 365

Glu Arg Gln Arg Ala Arg Ala Glu Glu Glu Glu Lys Ala Lys Val Glu
370 375 380

Glu Gln Lys Arg Asn Lys Gln Leu Glu Glu Lys Lys Arg Ala Met Gln
385 390 395 400

54/335

Glu Thr Lys Ile Lys Gly Glu Lys Val Glu Gln Lys Ile Glu Gly Lys
405 410 415

Trp Val Asn Glu Lys Lys Ala Gln Glu Asp Lys Leu Gln Thr Ala Val
420 425 430

5 Leu Lys Lys Gln Gly Glu Glu Lys Gly Thr Lys Val Gln Ala Lys Arg
435 440 445

Glu Lys Leu Gln Glu Asp Lys Pro Thr Phe Lys Lys Glu Glu Ile Lys
450 455 460

Asp Glu Lys Ile Lys Lys Asp Lys Glu Pro Lys Glu Glu Val Lys Ser
10 465 470 475 480

Phe Met Asp Arg Lys Lys Gly Phe Thr Glu Val Lys Ser Gln Asn Gly
485 490 495

Glu Phe Met Thr His Lys Leu Lys His Thr Glu Asn Thr Phe Ser Arg
500 505 510

15 Pro Gly Gly Arg Ala Ser Val Asp Thr Lys Glu Ala Glu Gly Ala Pro
515 520 525

Gln Val Glu Ala Gly Lys Arg Leu Glu Glu Leu Arg Arg Arg Gly
530 535 540

Glu Thr Glu Ser Glu Glu Phe Glu Lys Leu Lys Gln Lys Gln Gln Glu
20 545 550 555 560

Ala Ala Leu Glu Leu Glu Glu Leu Lys Lys Lys Arg Glu Glu Arg Arg
565 570 575

Lys Val Leu Glu Glu Glu Glu Gln Arg Arg Lys Gln Glu Glu Ala Asp
580 585 590

55/335

Arg Lys Leu Arg Glu Glu Glu Glu Lys Arg Arg Leu Lys Glu Glu Ile
595 600 605

Glu Arg Arg Arg Ala Glu Ala Ala Glu Lys Arg Gln Lys Met Pro Glu
610 615 620

5 Asp Gly Leu Ser Asp Asp Lys Lys Pro Phe Lys Cys Phe Thr Pro Lys
625 630 635 640

Gly Ser Ser Leu Lys Ile Glu Glu Arg Ala Glu Phe Leu Asn Lys Ser
645 650 655

Val Gln Lys Ser Ser Gly Val Lys Ser Thr His Gln Ala Ala Ile Val
10 660 665 670

Ser Lys Ile Asp Ser Arg Leu Glu Gln Tyr Thr Ser Ala Ile Glu Gly
675 680 685

Thr Lys Ser Ala Lys Pro Thr Lys Pro Ala Ala Ser Asp Leu Pro Val
690 695 700

15 Pro Ala Glu Gly Val Arg Asn Ile Lys Ser Met Trp Glu Lys Gly Asn
705 710 715 720

Val Phe Ser Ser Pro Thr Ala Ala Gly Thr Pro Asn Lys Glu Thr Ala
725 730 735

Gly Leu Lys Val Gly Val Ser Ser Arg Ile Asn Glu Trp Leu Thr Lys
20 740 745 750

Thr Pro Asp Gly Asn Lys Ser Pro Ala Pro Lys Pro Ser Asp Leu Arg
755 760 765

Pro Gly Asp Val Ser Ser Lys Arg Asn Leu Trp Glu Lys Gln Ser Val
770 775 780

Asp Lys Val Thr Ser Pro Thr Lys Val

785

790

5 <210> 13

<211> 458

<212> PRT

<213> Homo sapiens

<220>

10 <221> Alpha enolase

<222> (1)..(458)

<223> Accession No. as of 06 Dec 2002: Q05524

<400> 13

15 Met Ser Ile Leu Lys Ile Ile His Ala Arg Asp Ile Phe Glu Ser Arg

1

5

10

15

Gly Asn Pro Thr Val Glu Val Asp Leu Tyr Thr Asn Lys Gly Gly Leu

20

25

30

Phe Gly Arg Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu

20

35

40

45

Ala Leu Leu Glu Leu Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Gly

50

55

60

Lys Gly Val Ser Lys Ala Val Glu His Ile Ile Asn Lys Thr Ile Ala

65

70

75

80

57/335

Pro Ala Leu Ile Ser Lys Asn Val Asn Val Val Glu Gln Asp Lys Ile
85 90 95

Asp Asn Leu Met Leu Asp Met Asp Gly Ser Glu Asn Lys Ser Lys Phe
100 105 110

5 Gly Ala Asn Ala Ile Leu Gly Val Ser Leu Ala Val Cys Ser Asn Ala
115 120 125

Gly Ala Thr Ala Glu Lys Gly Val Pro Leu Tyr Arg His Ile Ala Asp
130 135 140

Leu Ala Gly Asn Asn Pro Glu Val Ile Leu Pro Val Pro Ala Phe Asn
10 145 150 155 160

Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu
165 170 175

Phe Met Ile Pro Pro Cys Gly Ala Asp Arg Phe Asn Asp Ala Ile Arg
180 185 190

15 Ile Gly Ala Glu Val Tyr His Asn Leu Lys Asn Val Ile Lys Glu Lys
195 200 205

Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro
210 215 220

Asn Ile Leu Glu Asn Lys Glu Ala Leu Glu Leu Leu Lys Thr Ala Ile
20 225 230 235 240

Gly Lys Ala Gly Tyr Ser Asp Lys Val Val Ile Gly Met Asp Val Ala
245 250 255

Ala Ser Glu Phe Tyr Arg Asp Gly Lys Tyr Asp Leu Asp Phe Asn Ser
260 265 270

Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro Asp Gln Leu Ala Asp Leu
275 280 285

Tyr Lys Gly Phe Val Leu Gly His Ala Val Lys Asn Tyr Pro Val Gly
290 295 300

5 Val Ser Ile Glu Asp Pro Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp
305 310 315 320

Lys Lys Leu Phe Thr Gly Ser Leu Val Gly Ile Gln Val Val Gly Asp
325 330 335

Asp Leu Thr Val Thr Lys Pro Glu Ala Arg Ile Ala Lys Ala Val Glu
10 340 345 350

Glu Val Lys Ala Cys Asn Cys Leu Leu Leu Lys Val Asn Gln Ile
355 360 365

Gly Ser Val Thr Glu Ser Leu Gln Ala Cys Lys Leu Ala Gln Ser Asn
370 375 380

15 Gly Trp Gly Val Met Pro Val Ser His Arg Leu Ser Gly Glu Thr Glu
385 390 395 400

Asp Thr Phe Met Ala Asp Leu Val Val Gly Leu Cys Thr Gly Gln Ile
405 410 415

Lys Thr Gly Pro Thr Cys Arg Ser Glu Arg Leu Ala Lys Tyr Asn Gln
20 420 425 430

Leu Leu Arg Ile Glu Glu Ala Glu Ala Gly Ser Lys Ala Arg Phe Ala
435 440 445

Gly Arg Asn Phe Arg Asn Pro Arg Ile Asn
450 455

<210> 14
<211> 408
5 <212> PRT
<213> Homo sapiens
<220>
<221> Aminoacylase-1
<222> (1)..(408)
10 <223> Accession No. as of 06 Dec 2002: Q03154
<400> 14

Met Thr Ser Lys Gly Pro Glu Glu Glu His Pro Ser Val Thr Leu Phe
1 5 10 15
15 Arg Gln Tyr Leu Arg Ile Arg Thr Val Gln Pro Lys Pro Asp Tyr Gly
20 25 30
Ala Ala Val Ala Phe Phe Glu Glu Thr Ala Arg Gln Leu Gly Leu Gly
35 40 45
Cys Gln Lys Val Glu Val Ala Pro Gly Tyr Val Val Thr Val Leu Thr
20 50 55 60
Trp Pro Gly Thr Asn Pro Thr Leu Ser Ser Ile Leu Leu Asn Ser His
65 70 75 80
Thr Asp Val Val Pro Val Phe Lys Glu His Trp Ser His Asp Pro Phe
85 90 95

60/335

Glu Ala Phe Lys Asp Ser Glu Gly Tyr Ile Tyr Ala Arg Gly Ala Gln
100 105 110

Asp Met Lys Cys Val Ser Ile Gln Tyr Leu Glu Ala Val Arg Arg Leu
115 120 125

5 Lys Val Glu Gly His Arg Phe Pro Arg Thr Ile His Met Thr Phe Val
130 135 140

Pro Asp Glu Glu Val Gly Gly His Gln Gly Met Glu Leu Phe Val Gln
145 150 155 160

Arg Pro Glu Phe His Ala Leu Arg Ala Gly Phe Ala Leu Asp Glu Gly
10 165 170 175

Ile Ala Asn Pro Thr Asp Ala Phe Thr Val Phe Tyr Ser Glu Arg Ser
180 185 190

Pro Trp Trp Val Arg Val Thr Ser Thr Gly Arg Pro Gly His Ala Ser
195 200 205

15 Arg Phe Met Glu Asp Thr Ala Ala Glu Lys Leu His Lys Val Val Asn
210 215 220

Ser Ile Leu Ala Phe Arg Glu Lys Glu Trp Gln Arg Leu Gln Ser Asn
225 230 235 240

Pro His Leu Lys Glu Gly Ser Val Thr Ser Val Asn Leu Thr Lys Leu
20 245 250 255

Glu Gly Gly Val Ala Tyr Asn Val Ile Pro Ala Thr Met Ser Ala Ser
260 265 270

Phe Asp Phe Arg Val Ala Pro Asp Val Asp Phe Lys Ala Phe Glu Glu
275 280 285

61/335

Gln Leu Gln Ser Trp Cys Gln Ala Ala Gly Glu Gly Val Thr Leu Glu
290 295 300
Phe Ala Gln Lys Trp Met His Pro Gln Val Thr Pro Thr Asp Asp Ser
305 310 315 320
5 Asn Pro Trp Trp Ala Ala Phe Ser Arg Val Cys Lys Asp Met Asn Leu
325 330 335
Thr Leu Glu Pro Glu Ile Met Pro Ala Ala Thr Asp Asn Arg Tyr Ile
340 345 350
Arg Ala Val Gly Val Pro Ala Leu Gly Phe Ser Pro Met Asn Arg Thr
10 355 360 365
Pro Val Leu Leu His Asp His Asp Glu Arg Leu His Glu Ala Val Phe
370 375 380
Leu Arg Gly Val Asp Ile Tyr Thr Arg Leu Leu Pro Ala Leu Ala Ser
385 390 395 400
15 Val Pro Ala Leu Pro Ser Asp Ser
405

<210> 15

20 <211> 277

<212> PRT

<213> Homo sapiens

<220>

<221> F-actin capping protein beta subunit

<222> (1)..(277)

<223> Accession No. as of 06 Dec 2002: P47756

<400> 15

5 Met Ser Asp Gln Gln Leu Asp Cys Ala Leu Asp Leu Met Arg Arg Leu
1 5 10 15
Pro Pro Gln Gln Ile Glu Lys Asn Leu Ser Asp Leu Ile Asp Leu Val
20 25 30
Pro Ser Leu Cys Glu Asp Leu Leu Ser Ser Val Asp Gln Pro Leu Lys
10 35 40 45
Ile Ala Arg Asp Lys Val Val Gly Lys Asp Tyr Leu Leu Cys Asp Tyr
50 55 60
Asn Arg Asp Gly Asp Ser Tyr Arg Ser Pro Trp Ser Asn Lys Tyr Asp
65 70 75 80
15 Pro Pro Leu Glu Asp Gly Ala Met Pro Ser Ala Arg Leu Arg Lys Leu
85 90 95
Glu Val Glu Ala Asn Asn Ala Phe Asp Gln Tyr Arg Asp Leu Tyr Phe
100 105 110
Glu Gly Gly Val Ser Ser Val Tyr Leu Trp Asp Leu Asp His Gly Phe
20 115 120 125
Ala Gly Val Ile Leu Ile Lys Lys Ala Gly Asp Gly Ser Lys Lys Ile
130 135 140
Lys Gly Cys Trp Asp Ser Ile His Val Val Glu Val Gln Glu Lys Ser
145 150 155 160

63/335

Ser Gly Arg Thr Ala His Tyr Lys Leu Thr Ser Thr Val Met Leu Trp
165 170 175
Leu Gln Thr Asn Lys Ser Gly Ser Gly Thr Met Asn Leu Gly Gly Ser
180 185 190
5 Leu Thr Arg Gln Met Glu Lys Asp Glu Thr Val Ser Asp Cys Ser Pro
195 200 205
His Ile Ala Asn Ile Gly Arg Leu Val Glu Asp Met Glu Asn Lys Ile
210 215 220
Arg Ser Thr Leu Asn Glu Ile Tyr Phe Gly Lys Thr Lys Asp Ile Val
10 225 230 235 240
Asn Gly Leu Arg Ser Ile Asp Ala Ile Pro Asp Asn Gln Lys Phe Lys
245 250 255
Gln Leu Gln Arg Glu Leu Ser Gln Val Leu Thr Gln Arg Gln Ile Tyr
260 265 270
15 Ile Gln Pro Asp Asn
275

<210> 16
20 <211> 289
<212> PRT
<213> Homo sapiens
<220>
<221> Inorganic pyrophosphatase

<222> (1)..(289)

<223> Accession No. as of 06 Dec 2002: Q15181

<400> 16

5 Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu
1 5 10 15
Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
20 25 30
His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val
10 35 40 45
Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp
50 55 60
Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr
65 70 75 80
15 Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala
85 90 95
Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly
100 105 110
Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys
20 115 120 125
Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu
130 135 140
Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn
145 150 155 160

65/335

Val Asp Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys
165 170 175
Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg
180 185 190
5 Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala
195 200 205
Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His
210 215 220
Asp His Trp Lys Ala Leu Val Thr Lys Lys Thr Asn Gly Lys Gly Ile
10 225 230 235 240
Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro
245 250 255
Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser
260 265 270
15 Ala Cys Thr Val Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys
275 280 285
Asn

20

<210> 17

<211> 250

<212> PRT

<213> Homo sapiens

<220>

<221> Galectin-3 (Galactose-specific lectin 3)

<222> (1)..(250)

<223> Accession No. as of 06 Dec 2002: P17931

5 <400> 17

Met Ala Asp Asn Phe Ser Leu His Asp Ala Leu Ser Gly Ser Gly Asn

1 5 10 15

Pro Asn Pro Gln Gly Trp Pro Gly Ala Trp Gly Asn Gln Pro Ala Gly

10 20 25 30

Ala Gly Gly Tyr Pro Gly Ala Ser Tyr Pro Gly Ala Tyr Pro Gly Gln

35 40 45

Ala Pro Pro Gly Ala Tyr Pro Gly Gln Ala Pro Pro Gly Ala Tyr His

50 55 60

15 Gly Ala Pro Gly Ala Tyr Pro Gly Ala Pro Ala Pro Gly Val Tyr Pro

65 70 75 80

Gly Pro Pro Ser Gly Pro Gly Ala Tyr Pro Ser Ser Gly Gln Pro Ser

85 90 95

Ala Pro Gly Ala Tyr Pro Ala Thr Gly Pro Tyr Gly Ala Pro Ala Gly

20 100 105 110

Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu Pro Gly Gly Val Val Pro

115 120 125

Arg Met Leu Ile Thr Ile Leu Gly Thr Val Lys Pro Asn Ala Asn Arg

130 135 140

67/335

Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp Val Ala Phe His Phe Asn
145 150 155 160
Pro Arg Phe Asn Glu Asn Asn Arg Arg Val Ile Val Cys Asn Thr Lys
165 170 175
5 Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg Gln Ser Val Phe Pro Phe
180 185 190
Glu Ser Gly Lys Pro Phe Lys Ile Gln Val Leu Val Glu Pro Asp His
195 200 205
Phe Lys Val Ala Val Asn Asp Ala His Leu Leu Gln Tyr Asn His Arg
10 210 215 220
Val Lys Lys Leu Asn Glu Ile Ser Lys Leu Gly Ile Ser Gly Asp Ile
225 230 235 240
Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile
245 250
15

<210> 18

<211> 347

<212> PRT

20 <213> Homo sapiens

<220>

<221> Voltage-dependent anion-selective channel protein 2 (VDAC-2)

<222> (1)..(347)

<223> Accession No.as of 06 Dec 2002: P45880

68/335

<400> 18

Met Ser Trp Cys Asn Glu Leu Arg Leu Pro Ala Leu Lys Gln His Ser
1 5 10 15
5 Ile Gly Arg Gly Leu Glu Ser His Ile Thr Met Cys Ile Pro Pro Ser
20 25 30
Tyr Ala Asp Leu Gly Lys Ala Ala Arg Asp Ile Phe Asn Lys Gly Phe
35 40 45
Gly Phe Gly Leu Val Lys Leu Asp Val Lys Thr Lys Ser Cys Ser Gly
10 50 55 60
Val Glu Phe Ser Thr Ser Gly Ser Ser Asn Thr Asp Thr Gly Lys Val
65 70 75 80
Thr Gly Thr Leu Glu Thr Lys Tyr Lys Trp Cys Glu Tyr Gly Leu Thr
85 90 95
15 Phe Thr Glu Lys Trp Asn Thr Asp Asn Thr Leu Gly Thr Glu Ile Ala
100 105 110
Ile Glu Asp Gln Ile Cys Gln Gly Leu Lys Leu Thr Phe Asp Thr Thr
115 120 125
Phe Ser Pro Asn Thr Gly Lys Lys Ser Gly Lys Ile Lys Ser Ser Tyr
20 130 135 140
Lys Arg Glu Cys Ile Asn Leu Gly Cys Asp Val Asp Phe Asp Phe Ala
145 150 155 160
Gly Pro Ala Ile His Gly Ser Ala Val Phe Gly Tyr Glu Gly Trp Leu
165 170 175

69/335

Ala Gly Tyr Gln Met Thr Phe Asp Ser Ala Lys Ser Lys Leu Thr Arg
180 185 190

Asn Asn Phe Ala Val Gly Tyr Arg Thr Gly Asp Phe Gln Leu His Thr
195 200 205

5 Asn Val Asn Asp Gly Thr Glu Phe Gly Gly Ser Ile Tyr Gln Lys Val
210 215 220

Cys Glu Asp Leu Asp Thr Ser Val Asn Leu Ala Trp Thr Ser Gly Thr
225 230 235 240

Asn Cys Thr Arg Phe Gly Ile Ala Ala Lys Tyr Gln Leu Asp Pro Thr
10 245 250 255

Ala Ser Ile Ser Ala Lys Val Asn Asn Ser Ser Leu Ile Gly Val Gly
260 265 270

Tyr Thr Gln Thr Leu Arg Pro Gly Val Lys Leu Thr Leu Ser Ala Leu
275 280 285

15 Val Asp Gly Lys Ser Ile Asn Ala Gly Gly His Lys Val Gly Ser Pro
290 295 300

Trp Ser Trp Arg Leu Asn Pro Ala Glu Arg Asn Leu Trp Glu Trp Ile
305 310 315 320

Ser Glu Asp Leu Ala Leu Ile Tyr Phe His Cys Asp Gln Gln Gln Ala
20 325 330 335

Phe Phe Pro Pro Glu Asp Asp Gln Asn Lys Gly
340 345

70/335

<210> 19

<211> 339

<212> PRT

<213> Homo sapiens

5 <220>

<221> Annexin II

<222> (1)..(339)

<223> Accession No. as of 06 Dec 2002: P07355

<400> 19

10

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp

1

5

10

15

His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn

20

25

30

15 Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr

35

40

45

Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser

50

55

60

Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys

20 65

70

75

80

Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu

85

90

95

Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser

100

105

110

71/335

Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu
115 120 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn
130 135 140

5 Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile
145 150 155 160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys
165 170 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp
10 180 185 190

Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr
195 200 205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His
210 215 220

15 Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met
225 230 235 240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe
245 250 255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp
20 260 265 270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu
275 280 285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg
290 295 300

72/335

Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln

305

310

315

320

Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly

325

330

335

5 Gly Asp Asp

<210> 20

10 <211> 418

<212> PRT

<213> Homo sapiens

<220>

<221> Collagen-binding protein 2 precursor

15 <222> (1)..(418)

<223> Accession No. as of 06 Dec 2002: P50454

<400> 20

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala

20 1

5

10

15

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr

20

25

30

Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala

35

40

45

Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val
 50 55 60
 Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu
 65 70 75 80
 5 Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val
 85 90 95
 Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly
 100 105 110
 Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp
 10 115 120 125
 Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp
 130 135 140
 Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys
 145 150 155 160
 15 Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp
 165 170 175
 Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val
 180 185 190
 Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro
 20 195 200 205
 His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe
 210 215 220
 Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr
 225 230 235 240

74/335

Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val
245 250 255

Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro
260 265 270

5 His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu
275 280 285

Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile
290 295 300

Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His
10 305 310 315 320

Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp
325 330 335

Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe
340 345 350

15 His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln
355 360 365

Asp Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala
370 375 380

Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu
20 385 390 395 400

Leu Phe Ile Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp
405 410 415

Glu Leu

<210> 21

<211> 166

5 <212> PRT

<213> Homo sapiens

<220>

<221> Cofilin, non-muscle isoform

<222> (1)..(166)

10 <223> Accession No. as of 08 ec 2002: P23528

<400> 21

Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn

1 5 10 15

15 Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg

20 25 30

Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile

35 40 45

Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val

20 50 55 60

Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys

65 70 75 80

Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys Lys

85 90 95

76/335

Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu Lys
100 105 110
Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Leu
115 120 125
5 Thr Gly Ile Lys His Glu Leu Gln Ala Asn Cys Tyr Glu Glu Val Lys
130 135 140
Asp Arg Cys Thr Leu Ala Glu Lys Leu Gly Gly Ser Ala Val Ile Ser
145 150 155 160
Leu Glu Gly Lys Pro Leu
10 165

<210> 22
<211> 165
15 <212> PRT
<213> Homo sapiens
<220>
<221> Peptidyl-prolyl cis-trans isomerase A
<222> (1)..(165)
20 <223> Accession No. as of 09 Dec 2002: P05092
<400> 22

Met Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val Asp Gly Glu Pro

77/335

Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro Lys Thr
20 25 30

Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Gly Tyr
35 40 45

5 Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly
50 55 60

Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly
65 70 75 80

Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His Thr Gly Pro Gly
10 85 90 95

Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe
100 105 110

Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Val
115 120 125

15 Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg
130 135 140

Phe Gly Ser Arg Asn Gly Lys Thr Ser Lys Lys Ile Thr Ile Ala Asp
145 150 155 160

Cys Gly Gln Leu Glu
20 165

<210> 23

<211> 638

<212> PRT

<213> Homo sapiens

<220>

<221> Dynein intermediate chain 2, cytosolic

5 <222> (1)..(638)

<223> Accession No. as of 09 Dec 2002: Q13409

<400> 23

Met Ser Asp Lys Ser Glu Leu Lys Ala Glu Leu Glu Arg Lys Lys Gln

10 1 5 10 15

Arg Leu Ala Gln Ile Arg Glu Glu Lys Lys Arg Lys Glu Glu Glu Arg

20 25 30

Lys Lys Lys Glu Thr Asp Gln Lys Lys Glu Ala Val Ala Pro Val Gln

35 40 45

15 Glu Glu Ser Asp Leu Glu Lys Lys Arg Arg Glu Ala Glu Ala Leu Leu

50 55 60

Gln Ser Met Gly Leu Thr Pro Glu Ser Pro Ile Val Phe Ser Glu Tyr

65 70 75 80

Trp Val Pro Pro Pro Met Ser Pro Ser Ser Lys Ser Val Ser Thr Pro

20 85 90 95

Ser Glu Ala Gly Ser Gln Asp Ser Gly Asp Gly Ala Val Gly Ser Arg

100 105 110

Thr Leu His Trp Asp Thr Asp Pro Ser Val Leu Gln Leu His Ser Asp

115 120 125

Ser Asp Leu Gly Arg Gly Pro Ile Lys Leu Gly Met Ala Lys Ile Thr
130 135 140

Gln Val Asp Phe Pro Pro Arg Glu Ile Val Thr Tyr Thr Lys Glu Thr
145 150 155 160

5 Gln Thr Pro Val Met Ala Gln Pro Lys Glu Asp Glu Glu Glu Asp Asp
165 170 175

Asp Val Val Ala Pro Lys Pro Pro Ile Glu Pro Glu Glu Glu Lys Thr
180 185 190

Leu Lys Lys Asp Glu Glu Asn Asp Ser Lys Ala Pro Pro His Glu Leu
10 195 200 205

Thr Glu Glu Glu Lys Gln Gln Ile Leu His Ser Glu Glu Phe Leu Ser
210 215 220

Phe Phe Asp His Ser Thr Arg Ile Val Glu Arg Ala Leu Ser Glu Gln
225 230 235 240

15 Ile Asn Ile Phe Phe Asp Tyr Ser Gly Arg Asp Leu Glu Asp Lys Glu
245 250 255

Gly Glu Ile Gln Ala Gly Ala Lys Leu Ser Leu Asn Arg Gln Phe Phe
260 265 270

Asp Glu Arg Trp Ser Lys His Arg Val Val Ser Cys Leu Asp Trp Ser
20 275 280 285

Ser Gln Tyr Pro Glu Leu Leu Val Ala Ser Tyr Asn Asn Asn Glu Asp
290 295 300

Ala Pro His Glu Pro Asp Gly Val Ala Leu Val Trp Asn Met Lys Tyr
305 310 315 320

80/335

Lys Lys Thr Thr Pro Glu Tyr Val Phe His Cys Gln Ser Ala Val Met
325 330 335

Ser Ala Thr Phe Ala Lys Phe His Pro Asn Leu Val Val Gly Gly Thr
340 345 350

5 Tyr Ser Gly Gln Ile Val Leu Trp Asp Asn Arg Ser Asn Lys Arg Thr
355 360 365

Pro Val Gln Arg Thr Pro Leu Ser Ala Ala Ala His Thr His Pro Val
370 375 380

Tyr Cys Val Asn Val Val Gly Thr Gln Asn Ala His Asn Leu Ile Ser
10 385 390 395 400

Ile Ser Thr Asp Gly Lys Ile Cys Ser Trp Ser Leu Asp Met Leu Ser
405 410 415

His Pro Gln Asp Ser Met Glu Leu Val His Lys Gln Ser Lys Ala Val
420 425 430

15 Ala Val Thr Ser Met Ser Phe Pro Val Gly Asp Val Asn Asn Phe Val
435 440 445

Val Gly Ser Glu Glu Gly Ser Val Tyr Thr Ala Cys Arg His Gly Ser
450 455 460

Lys Ala Gly Ile Ser Glu Met Phe Glu Gly His Gln Gly Pro Ile Thr
20 465 470 475 480

Gly Ile His Cys His Ala Ala Val Gly Ala Val Asp Phe Ser His Leu
485 490 495

Phe Val Thr Ser Ser Phe Asp Trp Thr Val Lys Leu Trp Thr Thr Lys
500 505 510

81/335

Asn Asn Lys Pro Leu Tyr Ser Phe Glu Asp Asn Ala Asp Tyr Val Tyr
515 520 525

Asp Val Met Trp Ser Pro Thr His Pro Ala Leu Phe Ala Cys Val Asp
530 535 540

5 Gly Met Gly Arg Leu Asp Leu Trp Asn Leu Asn Asn Asp Thr Glu Val
545 550 555 560

Pro Thr Ala Ser Ile Ser Val Glu Gly Asn Pro Ala Leu Asn Arg Val
565 570 575

Arg Trp Thr His Ser Gly Arg Glu Ile Ala Val Gly Asp Ser Glu Gly
10 580 585 590

Gln Ile Val Ile Tyr Asp Val Gly Glu Gln Ile Ala Val Pro Arg Asn
595 600 605

Asp Glu Trp Ala Arg Phe Gly Arg Thr Leu Ala Glu Ile Asn Ala Asn
610 615 620

15 Arg Ala Asp Ala Glu Glu Glu Ala Ala Thr Arg Ile Pro Ala
625 630 635

<210> 24

20 <211> 328

<212> PRT

<213> Homo sapiens

<220>

<221> Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor

<222> (1) .. (328)

<223> Accession No. as of 09 Dec 2002: Q13011

<400> 24

5 Met Ala Ala Gly Ile Val Ala Ser Arg Arg Leu Arg Asp Leu Leu Thr
1 5 10 15
Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg
20 25 30
Leu Thr Gly Ser Ser Ala Gln Glu Glu Ala Ser Gly Val Ala Leu Gly
10 35 40 45
Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln
50 55 60
Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys Arg Asn Ala
65 70 75 80
15 Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe Asn Lys Ile
85 90 95
Ser Arg Asp Ala Asp Cys Arg Ala Val Val Ile Ser Gly Ala Gly Lys
100 105 110
Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu
20 115 120 125
Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp
130 135 140
Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg Cys Pro
145 150 155 160

83/335

Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly Gly Val
165 170 175

Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe
180 185 190

5 Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val Gly Thr
195 200 205

Leu Glu Arg Leu Pro Lys Val Ile Gly Asn Gln Ser Leu Val Asn Glu
210 215 220

Leu Ala Phe Thr Ala His Lys Met Met Ala Asp Glu Ala Leu Asp Ser
10 225 230 235 240

Gly Leu Val Ser Arg Val Phe Pro Asp Lys Glu Val Met Leu Asp Ala
245 250 255

Ala Leu Pro Leu Ala Pro Glu Ile Ser Ser Lys Thr Thr Val Leu Val
260 265 270

15 Gln Ser Thr Lys Val Asn Leu Leu Tyr Ser Arg Asp His Ser Val Ala
275 280 285

Glu Ser Leu Asn Tyr Val Ala Ser Trp Asn Met Ser Met Leu Gln Thr
290 295 300

Gln Asp Leu Val Lys Ser Val Gln Pro Thr Thr Glu Asn Lys Glu Leu
20 305 310 315 320

Lys Thr Val Thr Phe Ser Lys Leu
325

<210> 25

<211> 1657

<212> PRT

<213> Homo sapiens

5 <220>

<221> Ras GTPase-activating-like protein IQGAP1

<222> (1)..(1657)

<223> Accession No. as of 09 Dec 2002: P46940

<400> 25

10

Met Ser Ala Ala Asp Glu Val Asp Gly Leu Gly Val Ala Arg Pro His

1 5 10 15

Tyr Gly Ser Val Leu Asp Asn Glu Arg Leu Thr Ala Glu Glu Met Asp

20 25 30

15 Glu Arg Arg Arg Gln Asn Val Ala Tyr Glu Tyr Leu Cys His Leu Glu

35 40 45

Glu Ala Lys Arg Trp Met Glu Ala Cys Leu Gly Glu Asp Leu Pro Pro

50 55 60

Thr Thr Glu Leu Glu Glu Gly Leu Arg Asn Gly Val Tyr Leu Ala Lys

20 65 70 75 80

Leu Gly Asn Phe Phe Ser Pro Lys Val Val Ser Leu Lys Lys Ile Tyr

85 90 95

Asp Arg Glu Gln Thr Arg Tyr Lys Ala Thr Gly Leu His Phe Arg His

100 105 110

85/335

Thr Asp Asn Val Ile Gln Trp Leu Asn Ala Met Asp Glu Ile Gly Leu
115 120 125

Pro Lys Ile Phe Tyr Pro Glu Thr Thr Asp Ile Tyr Asp Arg Lys Asn
130 135 140

5 Met Pro Arg Cys Ile Tyr Cys Ile His Ala Leu Ser Leu Tyr Leu Phe
145 150 155 160

Lys Leu Gly Leu Ala Pro Gln Ile Gln Asp Leu Tyr Gly Lys Val Asp
165 170 175

Phe Thr Glu Glu Glu Ile Asn Asn Met Lys Thr Glu Leu Glu Lys Tyr
10 180 185 190

Gly Ile Gln Met Pro Ala Phe Ser Lys Ile Gly Gly Ile Leu Ala Asn
195 200 205

Glu Leu Ser Val Asp Glu Ala Ala Leu His Ala Ala Val Ile Ala Ile
210 215 220

15 Asn Glu Ala Ile Asp Arg Arg Ile Pro Ala Asp Thr Phe Ala Ala Leu
225 230 235 240

Lys Asn Pro Asn Ala Met Leu Val Asn Leu Glu Glu Pro Leu Ala Ser
245 250 255

Thr Tyr Gln Asp Ile Leu Tyr Gln Ala Lys Gln Asp Lys Met Thr Asn
20 260 265 270

Ala Lys Asn Arg Thr Glu Asn Ser Glu Arg Glu Arg Asp Val Tyr Glu
275 280 285

Glu Leu Leu Thr Gln Ala Glu Ile Gln Gly Asn Ile Asn Lys Val Asn
290 295 300

86/335

Thr Phe Ser Ala Leu Ala Asn Ile Asp Leu Ala Leu Glu Gln Gly Asp
305 310 315 320
Ala Leu Ala Leu Phe Arg Ala Leu Gln Ser Pro Ala Leu Gly Leu Arg
325 330 335
5 Gly Leu Gln Gln Gln Asn Ser Asp Trp Tyr Leu Lys Gln Leu Leu Ser
340 345 350
Asp Lys Gln Gln Lys Arg Gln Ser Gly Gln Thr Asp Pro Leu Gln Lys
355 360 365
Glu Glu Leu Gln Ser Gly Val Asp Ala Ala Asn Ser Ala Ala Gln Gln
10 370 375 380
Tyr Gln Arg Arg Leu Ala Ala Val Ala Leu Ile Asn Ala Ala Ile Gln
385 390 395 400
Lys Gly Val Ala Glu Lys Thr Val Leu Glu Leu Met Asn Pro Glu Ala
405 410 415
15 Gln Leu Pro Gln Val Tyr Pro Phe Ala Ala Asp Leu Tyr Gln Lys Glu
420 425 430
Leu Ala Thr Leu Gln Arg Gln Ser Pro Glu His Asn Leu Thr His Pro
435 440 445
Glu Leu Ser Val Ala Val Glu Met Leu Ser Ser Val Ala Leu Ile Asn
20 450 455 460
Arg Ala Leu Glu Ser Gly Asp Val Asn Thr Val Trp Lys Gln Leu Ser
465 470 475 480
Ser Ser Val Thr Gly Leu Thr Asn Ile Glu Glu Glu Asn Cys Gln Arg
485 490 495

87/335

Tyr Leu Asp Glu Leu Met Lys Leu Lys Ala Gln Ala His Ala Glu Asn
500 505 510

Asn Glu Phe Ile Thr Trp Asn Asp Ile Gln Ala Cys Val Asp His Val
515 520 525

5 Asn Leu Val Val Gln Glu Glu His Glu Arg Ile Leu Ala Ile Gly Leu
530 535 540

Ile Asn Glu Ala Leu Asp Glu Gly Asp Ala Gln Lys Thr Leu Gln Ala
545 550 555 560

Leu Gln Ile Pro Ala Ala Lys Leu Glu Gly Val Leu Ala Glu Val Ala
10 565 570 575

Gln His Tyr Gln Asp Thr Leu Ile Arg Ala Lys Arg Glu Lys Ala Gln
580 585 590

Glu Ile Gln Asp Glu Ser Ala Val Leu Trp Leu Asp Glu Ile Gln Gly
595 600 605

15 Gly Ile Trp Gln Ser Asn Lys Asp Thr Gln Glu Ala Gln Lys Phe Ala
610 615 620

Leu Gly Ile Phe Ala Ile Asn Glu Ala Val Glu Ser Gly Asp Val Gly
625 630 635 640

Lys Thr Leu Ser Ala Leu Arg Ser Pro Asp Val Gly Leu Tyr Gly Val
20 645 650 655

Ile Pro Glu Cys Gly Glu Thr Tyr His Ser Asp Leu Ala Glu Ala Lys
660 665 670

Lys Lys Lys Leu Ala Val Gly Asp Asn Asn Ser Lys Trp Val Lys His
675 680 685

88/335

Trp Val Lys Gly Gly Tyr Tyr Tyr Tyr His Asn Leu Glu Thr Gln Glu
690 695 700

Gly Gly Trp Asp Glu Pro Pro Asn Phe Val Gln Asn Ser Met Gln Leu
705 710 715 720

5 Ser Arg Glu Glu Ile Gln Ser Ser Ile Ser Gly Val Thr Ala Ala Tyr
725 730 735

Asn Arg Glu Gln Leu Trp Leu Ala Asn Glu Gly Leu Ile Thr Arg Leu
740 745 750

Gln Ala Arg Cys Arg Gly Tyr Leu Val Arg Gln Glu Phe Arg Ser Arg
10 755 760 765

Met Asn Phe Leu Lys Lys Gln Ile Pro Ala Ile Thr Cys Ile Gln Ser
770 775 780

Gln Trp Arg Gly Tyr Lys Gln Lys Lys Ala Tyr Gln Asp Arg Leu Ala
785 790 795 800

15 Tyr Leu Arg Ser His Lys Asp Glu Val Val Lys Ile Gln Ser Leu Ala
805 810 815

Arg Met His Gln Ala Arg Lys Arg Tyr Arg Asp Arg Leu Gln Tyr Phe
820 825 830

Arg Asp His Ile Asn Asp Ile Ile Lys Ile Gln Ala Phe Ile Arg Ala
20 835 840 845

Asn Lys Ala Arg Asp Asp Tyr Lys Thr Leu Ile Asn Ala Glu Asp Pro
850 855 860

Pro Met Val Val Val Arg Lys Phe Val His Leu Leu Asp Gln Ser Asp
865 870 875 880

89/335

Gln Asp Phe Gln Glu Glu Leu Asp Leu Met Lys Met Arg Glu Glu Val
885 890 895

Ile Thr Leu Ile Arg Ser Asn Gln Gln Leu Glu Asn Asp Leu Asn Leu
900 905 910

5 Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Lys Ile Thr Leu Gln
915 920 925

Asp Val Val Ser His Ser Lys Lys Leu Thr Lys Lys Asn Lys Glu Gln
930 935 940

Leu Ser Asp Met Met Met Ile Asn Lys Gln Lys Gly Gly Leu Lys Ala
10 945 950 955 960

Leu Ser Lys Glu Lys Arg Glu Lys Leu Glu Ala Tyr Gln His Leu Phe
965 970 975

Tyr Leu Leu Gln Thr Asn Pro Thr Tyr Leu Ala Lys Leu Ile Phe Gln
980 985 990

15 Met Pro Gln Asn Lys Ser Thr Lys Phe Met Asp Ser Val Ile Phe Thr
995 1000 1005

Leu Tyr Asn Tyr Ala Ser Asn Gln Arg Glu Glu Tyr Leu Leu Leu
1010 1015 1020

Arg Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Lys Ser Lys Val
20 1025 1030 1035

Asp Gln Ile Gln Glu Ile Val Thr Gly Asn Pro Thr Val Ile Lys
1040 1045 1050

Met Val Val Ser Phe Asn Arg Gly Ala Arg Gly Gln Asn Ala Leu
1055 1060 1065

	Arg	Gln	Ile	Leu	Ala	Pro	Val	Val	Lys	Glu	Ile	Met	Asp	Asp	Lys
	1070						1075					1080			
	Ser	Leu	Asn	Ile	Lys	Thr	Asp	Pro	Val	Asp	Ile	Tyr	Lys	Ser	Trp
	1085						1090					1095			
5	Val	Asn	Gln	Met	Glu	Ser	Gln	Thr	Gly	Glu	Ala	Ser	Lys	Leu	Pro
	1100						1105					1110			
	Tyr	Asp	Val	Thr	Pro	Glu	Gln	Ala	Leu	Ala	His	Glu	Glu	Val	Lys
	1115						1120					1125			
	Thr	Arg	Leu	Asp	Ser	Ser	Ile	Arg	Asn	Met	Arg	Ala	Val	Thr	Asp
10	1130						1135					1140			
	Lys	Phe	Leu	Ser	Ala	Ile	Val	Ser	Ser	Val	Asp	Lys	Ile	Pro	Tyr
	1145						1150					1155			
	Gly	Met	Arg	Phe	Ile	Ala	Lys	Val	Leu	Lys	Asp	Ser	Leu	His	Glu
	1160						1165					1170			
15	Lys	Phe	Pro	Asp	Ala	Gly	Glu	Asp	Glu	Leu	Leu	Lys	Ile	Ile	Gly
	1175						1180					1185			
	Asn	Leu	Leu	Tyr	Tyr	Arg	Tyr	Met	Asn	Pro	Ala	Ile	Val	Ala	Pro
	1190						1195					1200			
	Asp	Ala	Phe	Asp	Ile	Ile	Asp	Leu	Ser	Ala	Gly	Gly	Gln	Leu	Thr
20	1205						1210					1215			
	Thr	Asp	Gln	Arg	Arg	Asn	Leu	Gly	Ser	Ile	Ala	Lys	Met	Leu	Gln
	1220						1225					1230			
	His	Ala	Ala	Ser	Asn	Lys	Met	Phe	Leu	Gly	Asp	Asn	Ala	His	Leu
	1235						1240					1245			

	Ser Ile	Ile Asn Glu Tyr Leu	Ser Gln Ser Tyr Gln	Lys Phe Arg
	1250		1255	1260
	Arg Phe	Phe Gln Thr Ala Cys	Asp Val Pro Glu Leu	Gln Asp Lys
	1265		1270	1275
5	Phe Asn	Val Asp Glu Tyr Ser	Asp Leu Val Thr Leu	Thr Lys Pro
	1280		1285	1290
	Val Ile	Tyr Ile Ser Ile Gly	Glu Ile Ile Asn Thr	His Thr Leu
	1295		1300	1305
	Leu Leu	Asp His Gln Asp Ala	Ile Ala Pro Glu His	Asn Asp Pro
10	1310		1315	1320
	Ile His	Glu Leu Leu Asp Asp	Leu Gly Glu Val Pro	Thr Ile Glu
	1325		1330	1335
	Ser Leu	Ile Gly Glu Ser Ser	Gly Asn Leu Asn Asp	Pro Asn Lys
	1340		1345	1350
15	Glu Ala	Leu Ala Lys Thr Glu	Val Ser Leu Thr Leu	Thr Asn Lys
	1355		1360	1365
	Phe Asp	Val Pro Gly Asp Glu	Asn Ala Glu Met Asp	Ala Arg Thr
	1370		1375	1380
	Ile Leu	Leu Asn Thr Lys Arg	Leu Ile Val Asp Val	Ile Arg Phe
20	1385		1390	1395
	Gln Pro	Gly Glu Thr Leu Thr	Glu Ile Leu Glu Thr	Pro Ala Thr
	1400		1405	1410
	Ser Glu	Gln Glu Ala Glu His	Gln Arg Ala Met Gln	Arg Arg Ala
	1415		1420	1425

	Ile Arg	Asp Ala Lys Thr Pro	Asp Lys Met Lys Lys	Ser Lys Ser
	1430	1435	1440	
	Val Lys	Glu Asp Ser Asn Leu	Thr Leu Gln Glu Lys	Lys Glu Lys
	1445	1450	1455	
5	Ile Gln	Thr Gly Leu Lys Lys	Leu Thr Glu Leu Gly	Thr Val Asp
	1460	1465	1470	
	Pro Lys	Asn Lys Tyr Gln Glu	Leu Ile Asn Asp Ile	Ala Arg Asp
	1475	1480	1485	
	Ile Arg	Asn Gln Arg Arg Tyr	Arg Gln Arg Arg Lys	Ala Glu Leu
10	1490	1495	1500	
	Val Lys	Leu Gln Gln Thr Tyr	Ala Ala Leu Asn Ser	Lys Ala Thr
	1505	1510	1515	
	Phe Tyr	Gly Glu Gln Val Asp	Tyr Tyr Lys Ser Tyr	Ile Lys Thr
	1520	1525	1530	
15	Cys Leu	Asp Asn Leu Ala Ser	Lys Gly Lys Val Ser	Lys Lys Pro
	1535	1540	1545	
	Arg Glu	Met Lys Gly Lys Lys	Ser Lys Lys Ile Ser	Leu Lys Tyr
	1550	1555	1560	
	Thr Ala	Ala Arg Leu His Glu	Lys Gly Val Leu Leu	Glu Ile Glu
20	1565	1570	1575	
	Asp Leu	Gln Val Asn Gln Phe	Lys Asn Val Ile Phe	Glu Ile Ser
	1580	1585	1590	
	Pro Thr	Glu Glu Val Gly Asp	Phe Glu Val Lys Ala	Lys Phe Met
	1595	1600	1605	

93/335

Gly Val Gln Met Glu Thr Phe Met Leu His Tyr Gln Asp Leu Leu

1610

1615

1620

Gln Leu Gln Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asp Arg

1625

1630

1635

5 Ala Lys Val Asn Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys

1640

1645

1650

Phe Tyr Gly Lys

1655

10

<210> 26

<211> 627

<212> PRT

<213> Homo sapiens

15 <220>

<221> L-plastin (Lymphocyte cytosolic protein 1)

<222> (1)..(627)

<223> Accession No. as of 09 Dec 2002: P13796

20 <400> 26

Met Ala Arg Gly Ser Val Ser Asp Glu Glu Met Met Glu Leu Arg Glu

1

5

10

15

Ala Phe Ala Lys Val Asp Thr Asp Gly Asn Gly Tyr Ile Ser Phe Asn

94/335

20 25 30
Glu Leu Asn Asp Leu Phe Lys Ala Ala Cys Leu Pro Leu Pro Gly Tyr
35 40 45
Arg Val Arg Glu Ile Thr Glu Asn Leu Met Ala Thr Gly Asp Leu Asp
5 50 55 60
Gln Asp Gly Arg Ile Ser Phe Asp Glu Phe Ile Lys Ile Phe His Gly
65 70 75 80
Leu Lys Ser Thr Asp Val Ala Lys Thr Phe Arg Lys Ala Ile Asn Lys
85 90 95
10 Lys Glu Gly Ile Cys Ala Ile Gly Gly Thr Ser Glu Gln Ser Ser Val
100 105 110
Gly Thr Gln His Ser Tyr Ser Glu Glu Glu Lys Tyr Ala Phe Val Asn
115 120 125
Trp Ile Asn Lys Ala Leu Glu Asn Asp Pro Asp Cys Arg His Val Ile
15 130 135 140
Pro Met Asn Pro Asn Thr Asn Asp Leu Phe Asn Ala Val Gly Asp Gly
145 150 155 160
Ile Val Leu Cys Lys Met Ile Asn Leu Ser Val Pro Asp Thr Ile Asp
165 170 175
20 Glu Arg Thr Ile Asn Lys Lys Lys Leu Thr Pro Phe Thr Ile Gln Glu
180 185 190
Asn Leu Asn Leu Ala Leu Asn Ser Ala Ser Ala Ile Gly Cys His Val
195 200 205
Val Asn Ile Gly Ala Glu Asp Leu Lys Glu Gly Lys Pro Tyr Leu Val

95/335

210 215 220
Leu Gly Leu Leu Trp Gln Val Ile Lys Ile Gly Leu Phe Ala Asp Ile
225 230 235 240
Glu Leu Ser Arg Asn Glu Ala Leu Ile Ala Leu Leu Arg Glu Gly Glu
5 245 250 255
Ser Leu Glu Asp Leu Met Lys Leu Ser Pro Glu Glu Leu Leu Leu Arg
260 265 270
Trp Ala Asn Tyr His Leu Glu Asn Ala Gly Cys Asn Lys Ile Gly Asn
275 280 285
10 Phe Ser Thr Asp Ile Lys Asp Ser Lys Ala Tyr Tyr His Leu Leu Glu
290 295 300
Gln Val Ala Pro Lys Gly Asp Glu Glu Gly Val Pro Ala Val Val Ile
305 310 315 320
Asp Met Ser Gly Leu Arg Glu Lys Asp Asp Ile Gln Arg Ala Glu Cys
15 325 330 335
Met Leu Gln Gln Ala Glu Arg Leu Gly Cys Arg Gln Phe Val Thr Ala
340 345 350
Thr Asp Val Val Arg Gly Asn Pro Lys Leu Asn Leu Ala Phe Ile Ala
355 360 365
20 Asn Leu Phe Asn Arg Tyr Pro Ala Leu His Lys Pro Glu Asn Gln Asp
370 375 380
Ile Asp Trp Gly Ala Leu Glu Gly Glu Thr Arg Glu Glu Arg Thr Phe
385 390 395 400
Arg Asn Trp Met Asn Ser Leu Gly Val Asn Pro Arg Val Asn His Leu

96/335

	405	410	415
	Tyr Ser Asp Leu Ser Asp Ala Leu Val Ile Phe Gln Leu Tyr Glu Lys		
	420	425	430
	Ile Lys Val Pro Val Asp Trp Asn Arg Val Asn Lys Pro Pro Tyr Pro		
5	435	440	445
	Lys Leu Gly Gly Asn Met Lys Lys Leu Glu Asn Cys Asn Tyr Ala Val		
	450	455	460
	Glu Leu Gly Lys Asn Gln Ala Lys Phe Ser Leu Val Gly Ile Gly Gly		
	465	470	475 480
10	Gln Asp Leu Asn Glu Gly Asn Arg Thr Leu Thr Leu Ala Leu Ile Trp		
	485	490	495
	Gln Leu Met Arg Arg Tyr Thr Leu Asn Ile Leu Glu Glu Ile Gly Gly		
	500	505	510
	Gly Gln Lys Val Asn Asp Asp Ile Ile Val Asn Trp Val Asn Glu Thr		
15	515	520	525
	Leu Arg Glu Ala Glu Lys Ser Ser Ser Ile Ser Ser Phe Lys Asp Pro		
	530	535	540
	Lys Ile Ser Thr Ser Leu Pro Val Leu Asp Leu Ile Asp Ala Ile Gln		
	545	550	555 560
20	Pro Gly Ser Ile Asn Tyr Asp Leu Leu Lys Thr Glu Asn Leu Asn Asp		
	565	570	575
	Asp Glu Lys Leu Asn Asn Ala Lys Tyr Ala Ile Ser Met Ala Arg Lys		
	580	585	590
	Ile Gly Ala Arg Val Tyr Ala Leu Pro Glu Asp Leu Val Glu Val Asn		

97/335

595

600

605

Pro Lys Met Val Met Thr Val Phe Ala Cys Leu Met Gly Lys Gly Met

610

615

620

Lys Arg Val

5 625

<210> 27

<211> 216

10 <212> PRT

<213> Homo sapiens

<220>

<221> GTP-binding nuclear protein RAN

<222> (1)..(216)

15 <223> Accession No. as of 09 Dec 2002: P17080

<400> 27

Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val

1

5

10

15

20 Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr

20

25

30

Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His

35

40

45

Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp

98/335

50 55 60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
65 70 75 80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
5 85 90 95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
100 105 110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
115 120 125
10 Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
130 135 140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
145 150 155 160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
15 165 170 175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
180 185 190
Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
195 200 205
20 Leu Pro Asp Glu Asp Asp Asp Leu
210 215

<211> 463

<212> PRT

<213> Homo sapiens

<220>

5 <221> Heterogeneous nuclear ribonucleoprotein K

<222> (1)..(463)

<223> Accession No. as of 09 Dec 2002: Q07244

<400> 28

10 Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn

1 5 10 15

Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala

20 25 30

Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu

15 35 40 45

Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn

50 55 60

Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp

65 70 75 80

20 Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr

85 90 95

Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu

100 105 110

Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp

100/335

115 120 125
Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp

130 135 140
Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile

5 145 150 155 160
Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr

165 170 175
Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val

180 185 190
10 Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile

195 200 205
Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro

210 215 220
Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr

15 225 230 235 240
Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg

245 250 255
Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro

260 265 270
20 Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly

275 280 285
Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala

290 295 300
Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu

101/335

305 310 315 320
Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met
325 330 335
Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp
5 340 345 350
Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly
355 360 365
Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly
370 375 380
10 Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly
385 390 395 400
Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu
405 410 415
Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp
15 420 425 430
Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln
435 440 445
Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ser Gly Lys Phe Phe
450 455 460

20

<210> 29

<211> 172

<212> PRT

<213> Homo sapiens

<220>

<221> Translationally controlled tumor protein (TCTP)

<222> (1)..(172)

5 <223> Accession No. as of 09 Dec 2002: P13693

<400> 29

Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp

1 5 10 15

10 Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu

20 25 30

Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile

35 40 45

Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser

15 50 55 60

Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu

65 70 75 80

Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met

85 90 95

20 Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys

100 105 110

Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn

115 120 125

Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly

103/335

130 135 140
Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met
145 150 155 160
Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
5 165 170

<210> 30
<211> 284
10 <212> PRT
<213> Homo sapiens
<220>
<221> Tropomyosin 1 alpha chain
<222> (1)..(284)
15 <223> Accession No. as of 06 Dec 2002: P09493
<400> 30

Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu
1 5 10 15
20 Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala
20 25 30
Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys
35 40 45
Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu

104/335

50 55 60
Lys Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp
65 70 75 80
Ala Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu
5 85 90 95
Glu Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys
100 105 110
Leu Glu Glu Ala Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys
115 120 125
10 Val Ile Glu Ser Arg Ala Gln Lys Asp Glu Glu Lys Met Glu Ile Gln
130 135 140
Glu Ile Gln Leu Lys Glu Ala Lys His Ile Ala Glu Asp Ala Asp Arg
145 150 155 160
Lys Tyr Glu Glu Val Ala Arg Lys Leu Val Ile Ile Glu Ser Asp Leu
15 165 170 175
Glu Arg Ala Glu Glu Arg Ala Glu Leu Ser Glu Gly Lys Cys Ala Glu
180 185 190
Leu Glu Glu Glu Leu Lys Thr Val Thr Asn Asn Leu Lys Ser Leu Glu
195 200 205
20 Ala Gln Ala Glu Lys Tyr Ser Gln Lys Glu Asp Arg Tyr Glu Glu Glu
210 215 220
Ile Lys Val Leu Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu
225 230 235 240
Phe Ala Glu Arg Ser Val Thr Lys Leu Glu Lys Ser Ile Asp Asp Leu

105/335

245 250 255
Glu Asp Glu Leu Tyr Ala Gln Lys Leu Lys Tyr Lys Ala Ile Ser Glu
260 265 270
Glu Leu Asp His Ala Leu Asn Asp Met Thr Ser Ile
5 275 280

<210> 31
<211> 482
10 <212> PRT
<213> Homo sapiens
<220>
<221> Thymidine phosphorylase precursor
<222> (1)..(482)
15 <223> Accession No. as of 09 Dec 2002: P19971
<400> 31

Met Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly
1 5 10 15
20 Asp Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu
20 25 30
Pro Lys Gln Leu Pro Glu Leu Ile Arg Met Lys Arg Asp Gly Gly Arg
35 40 45
Leu Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly

106/335

50 55 60
Ser Ala Gln Gly Ala Gln Ile Gly Ala Met Leu Met Ala Ile Arg Leu
65 70 75 80
Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln Ala Leu Ala
5 85 90 95
Gln Ser Gly Gln Gln Leu Glu Trp Pro Glu Ala Trp Arg Gln Gln Leu
100 105 110
Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Lys Val Ser Leu Val
115 120 125
10 Leu Ala Pro Ala Leu Ala Ala Cys Gly Cys Lys Val Pro Met Ile Ser
130 135 140
Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu Ser
145 150 155 160
Ile Pro Gly Phe Asn Val Ile Gln Ser Pro Glu Gln Met Gln Val Leu
15 165 170 175
Leu Asp Gln Ala Gly Cys Cys Ile Val Gly Gln Ser Glu Gln Leu Val
180 185 190
Pro Ala Asp Gly Ile Leu Tyr Ala Ala Arg Asp Val Thr Ala Thr Val
195 200 205
20 Asp Ser Leu Pro Leu Ile Thr Ala Ser Ile Leu Ser Lys Lys Leu Val
210 215 220
Glu Gly Leu Ser Ala Leu Val Val Asp Val Lys Phe Gly Gly Ala Ala
225 230 235 240
Val Phe Pro Asn Gln Glu Gln Ala Arg Glu Leu Ala Lys Thr Leu Val

107/335

245 250 255
Gly Val Gly Ala Ser Leu Gly Leu Arg Val Ala Ala Ala Leu Thr Ala

260 265 270
Met Asp Lys Pro Leu Gly Arg Cys Val Gly His Ala Leu Glu Val Glu

5 275 280 285
Glu Ala Leu Leu Cys Met Asp Gly Ala Gly Pro Pro Asp Leu Arg Asp

290 295 300
Leu Val Thr Thr Leu Gly Gly Ala Leu Leu Trp Leu Ser Gly His Ala

305 310 315 320
10 Gly Thr Gln Ala Gln Gly Ala Ala Arg Val Ala Ala Ala Leu Asp Asp

325 330 335
Gly Ser Ala Leu Gly Arg Phe Glu Arg Met Leu Ala Ala Gln Gly Val

340 345 350
Asp Pro Gly Leu Ala Arg Ala Leu Cys Ser Gly Ser Pro Ala Glu Arg

15 355 360 365
Arg Gln Leu Leu Pro Arg Ala Arg Glu Gln Glu Glu Leu Leu Ala Pro

370 375 380
Ala Asp Gly Thr Val Glu Leu Val Arg Ala Leu Pro Leu Ala Leu Val

385 390 395 400
20 Leu His Glu Leu Gly Ala Gly Arg Ser Arg Ala Gly Glu Pro Leu Arg

405 410 415
Leu Gly Val Gly Ala Glu Leu Leu Val Asp Val Gly Gln Arg Leu Arg

420 425 430
Arg Gly Thr Pro Trp Leu Arg Val His Arg Asp Gly Pro Ala Leu Ser

108/335

435

440

445

Gly Pro Gln Ser Arg Ala Leu Gln Glu Ala Leu Val Leu Ser Asp Arg

450

455

460

Ala Pro Phe Ala Ala Pro Leu Pro Phe Ala Glu Leu Val Leu Pro Pro

5 465

470

475

480

Gln Gln

10 <210> 32

<211> 488

<212> PRT

<213> Homo sapiens

<220>

15 <221> Cytosol aminopeptidase

<222> (1)..(488)

<223> Accession No. as of 09 Dec 2002: P28838

<400> 32

20 Met Thr Lys Gly Leu Val Leu Gly Ile Tyr Ser Lys Glu Lys Glu Asp

1

5

10

15

Asp Val Pro Gln Phe Thr Ser Ala Gly Glu Asn Phe Asp Lys Leu Leu

20

25

30

Ala Gly Lys Leu Arg Glu Thr Leu Asn Ile Ser Gly Pro Pro Leu Lys

109/335

35 40 45
Ala Gly Lys Thr Arg Thr Phe Tyr Gly Leu His Gln Asp Phe Pro Ser
50 55 60
Val Val Leu Val Gly Leu Gly Lys Lys Ala Ala Gly Ile Asp Glu Gln
5 65 70 75 80
Glu Asn Trp His Glu Gly Lys Glu Asn Ile Arg Ala Ala Val Ala Ala
85 90 95
Gly Cys Arg Gln Ile Gln Asp Leu Glu Leu Ser Ser Val Glu Val Asp
100 105 110
10 Pro Cys Gly Asp Ala Gln Ala Ala Ala Glu Gly Ala Val Leu Gly Leu
115 120 125
Tyr Glu Tyr Asp Asp Leu Lys Gln Lys Lys Lys Met Ala Val Ser Ala
130 135 140
Lys Leu Tyr Gly Ser Gly Asp Gln Glu Ala Trp Gln Lys Gly Val Leu
15 145 150 155 160
Phe Ala Ser Gly Gln Asn Leu Ala Arg Gln Leu Met Glu Thr Pro Ala
165 170 175
Asn Glu Met Thr Pro Thr Arg Phe Ala Glu Ile Ile Glu Lys Asn Leu
180 185 190
20 Lys Ser Ala Ser Ser Lys Thr Glu Val His Ile Arg Pro Lys Ser Trp
195 200 205
Ile Glu Glu Gln Ala Met Gly Ser Phe Leu Ser Val Ala Lys Gly Ser
210 215 220
Asp Glu Pro Pro Val Phe Leu Glu Ile His Tyr Lys Gly Ser Pro Asn

110/335

225 230 235 240
Ala Asn Glu Pro Pro Leu Val Phe Val Gly Lys Gly Ile Thr Phe Asp
 245 250 255
Ser Gly Gly Ile Ser Ile Lys Ala Ser Ala Asn Met Asp Leu Met Arg
5 260 265 270
Ala Asp Met Gly Gly Ala Ala Thr Ile Cys Ser Ala Ile Val Ser Ala
 275 280 285
Ala Lys Leu Asn Leu Pro Ile Asn Ile Ile Gly Leu Ala Pro Leu Cys
 290 295 300
10 Glu Asn Met Pro Ser Gly Lys Ala Asn Lys Pro Gly Asp Val Val Arg
 305 310 315 320
Ala Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly
 325 330 335
Arg Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro
15 340 345 350
Lys Val Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala
 355 360 365
Leu Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp
 370 375 380
20 Asn Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg
 385 390 395 400
Met Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu
 405 410 415
Ala Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr

111/335

420 425 430
Ala Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His
435 440 445
Leu Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu
5 450 455 460
Arg Lys Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu
465 470 475 480
Leu Arg Phe Ser Gln Asp Asn Ala
485

10

<210> 33
<211> 400
<212> PRT
15 <213> Homo sapiens
<220>
<221> Keratin, type I cytoskeletal 19
<222> (1)..(400)
<223> Accession No. as of 09 Dec 2002 : P08727

20

<400> 33

Met Thr Ser Tyr Ser Tyr Arg Gln Ser Ser Ala Thr Ser Ser Phe Gly

1

5

10

15

112/335

Gly Leu Gly Gly Gly Ser Val Arg Phe Gly Pro Gly Val Ala Phe Arg
20 25 30

Ala Pro Ser Ile His Gly Gly Ser Gly Gly Arg Gly Val Ser Val Ser
35 40 45

5 Ser Ala Arg Phe Val Ser Ser Ser Ser Ser Gly Gly Tyr Gly Gly Gly
50 55 60

Tyr Gly Gly Val Leu Thr Ala Ser Asp Gly Leu Leu Ala Gly Asn Glu
65 70 75 80

Lys Leu Thr Met Gln Asn Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp
10 85 90 95

Lys Val Arg Ala Leu Glu Ala Ala Asn Gly Glu Leu Glu Val Lys Ile
100 105 110

Arg Asp Trp Tyr Gln Lys Gln Gly Pro Gly Pro Ser Arg Asp Tyr Ser
115 120 125

15 His Tyr Tyr Thr Thr Ile Gln Asp Leu Arg Asp Lys Ile Leu Gly Ala
130 135 140

Thr Ile Glu Asn Ser Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu
145 150 155 160

Ala Ala Asp Asp Phe Arg Thr Lys Phe Glu Thr Glu Gln Ala Leu Arg
20 165 170 175

Met Ser Val Glu Ala Asp Ile Asn Gly Leu Arg Arg Val Leu Asp Glu
180 185 190

Leu Thr Leu Ala Arg Thr Asp Leu Glu Met Gln Ile Glu Gly Leu Lys
195 200 205

Glu Glu Leu Ala Tyr Leu Lys Lys Asn His Glu Glu Glu Ile Ser Thr
210 215 220
Leu Arg Gly Gln Val Gly Gly Gln Val Ser Val Glu Val Asp Ser Ala
225 230 235 240
5 Pro Gly Thr Asp Leu Ala Lys Ile Leu Ser Asp Met Arg Ser Gln Tyr
245 250 255
Glu Val Met Ala Glu Gln Asn Arg Lys Asp Ala Glu Ala Trp Phe Thr
260 265 270
Ser Arg Thr Glu Glu Leu Asn Arg Glu Val Ala Gly His Thr Glu Gln
10 275 280 285
Leu Gln Met Ser Arg Ser Glu Val Thr Asp Leu Arg Arg Thr Leu Gln
290 295 300
Gly Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala Ala Leu
305 310 315 320
15 Glu Asp Thr Leu Ala Glu Thr Glu Ala Arg Phe Gly Ala Gln Leu Ala
325 330 335
His Ile Gln Ala Leu Ile Ser Gly Ile Glu Ala Gln Leu Ala Asp Val
340 345 350
Arg Ala Asp Ser Glu Arg Gln Asn Gln Glu Tyr Gln Arg Leu Met Asp
20 355 360 365
Ile Lys Ser Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Ser Leu Leu
370 375 380
Glu Gly Gln Glu Asp His Tyr Asn Asn Leu Ser Ala Ser Lys Val Leu
385 390 395 400

<210> 34
<211> 325
5 <212> PRT
<213> Homo sapiens
<220>
<221> Alcohol dehydrogenase [NADP+]
<222> (1)..(325)
10 <223> Accession No. as of 09 Dec 2002: P14550
<400> 34

Met Ala Ala Ser Cys Val Leu Leu His Thr Gly Gln Lys Met Pro Leu
1 5 10 15
15 Ile Gly Leu Gly Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala
20 25 30
Val Lys Tyr Ala Leu Ser Val Gly Tyr Arg His Ile Asp Cys Ala Ala
35 40 45
Ile Tyr Gly Asn Glu Pro Glu Ile Gly Glu Ala Leu Lys Glu Asp Val
20 50 55 60
Gly Pro Gly Lys Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys
65 70 75 80
Leu Trp Asn Thr Lys His His Pro Glu Asp Val Glu Pro Ala Leu Arg
85 90 95

115/335

Lys Thr Leu Ala Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met
100 105 110

His Trp Pro Tyr Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn
115 120 125

5 Ala Asp Gly Thr Ile Cys Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp
130 135 140

Lys Ala Leu Glu Ala Leu Val Ala Lys Gly Leu Val Gln Ala Leu Gly
145 150 155 160

Leu Ser Asn Phe Asn Ser Arg Gln Ile Asp Asp Ile Leu Ser Val Ala
10 165 170 175

Ser Val Arg Pro Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala
180 185 190

Gln Asn Glu Leu Ile Ala His Cys Gln Ala Arg Gly Leu Glu Val Thr
195 200 205

15 Ala Tyr Ser Pro Leu Gly Ser Ser Asp Arg Ala Trp Arg Asp Pro Asp
210 215 220

Glu Pro Val Leu Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys
225 230 235 240

Tyr Gly Arg Ser Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg
20 245 250 255

Lys Val Ile Cys Ile Pro Lys Ser Ile Thr Pro Ser Arg Ile Leu Gln
260 265 270

Asn Ile Lys Val Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln
275 280 285

116/335

Leu Asn Ala Leu Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Leu Thr

290

295

300

Val Asp Gly Lys Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro

305

310

315

320

5 Phe Asn Asp Pro Tyr

325

<210> 35

10 <211> 270

<212> PRT

<213> Homo sapiens

<220>

<221> Elastase IIIA precursor

15 <222> (1)..(270)

<223> Accession No. as of 09 Dec 2002: P09093

<400> 35

Met Met Leu Arg Leu Leu Ser Ser Leu Leu Leu Val Ala Val Ala Ser

20 1

5

10

15

Gly Tyr Gly Pro Pro Ser Ser His Ser Ser Ser Arg Val Val His Gly

20

25

30

Glu Asp Ala Val Pro Tyr Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr

35

40

45

117/335

Glu Lys Ser Gly Ser Phe Tyr His Thr Cys Gly Gly Ser Leu Ile Ala
 50 55 60
 Pro Asp Trp Val Val Thr Ala Gly His Cys Ile Ser Arg Asp Leu Thr
 65 70 75 80
 5 Tyr Gln Val Val Leu Gly Glu Tyr Asn Leu Ala Val Lys Glu Gly Pro
 85 90 95
 Glu Gln Val Ile Pro Ile Asn Ser Glu Glu Leu Phe Val His Pro Leu
 100 105 110
 Trp Asn Arg Ser Cys Val Ala Cys Gly Asn Asp Ile Ala Leu Ile Lys
 10 115 120 125
 Leu Ser Arg Ser Ala Gln Leu Gly Asp Ala Val Gln Leu Ala Ser Leu
 130 135 140
 Pro Pro Ala Gly Asp Ile Leu Pro Asn Lys Thr Pro Cys Tyr Ile Thr
 145 150 155 160
 15 Gly Trp Gly Arg Leu Tyr Thr Asn Gly Pro Leu Pro Asp Lys Leu Gln
 165 170 175
 Gln Ala Arg Leu Pro Val Val Asp Tyr Lys His Cys Ser Arg Trp Asn
 180 185 190
 Trp Trp Gly Ser Thr Val Lys Lys Thr Met Val Cys Ala Gly Gly Tyr
 20 195 200 205
 Ile Arg Ser Gly Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Pro
 210 215 220
 Thr Glu Asp Gly Gly Trp Gln Val His Gly Val Thr Ser Phe Val Ser
 225 230 235 240

118/335

Gly Phe Gly Cys Asn Phe Ile Trp Lys Pro Thr Val Phe Thr Arg Val

245

250

255

Ser Ala Phe Ile Asp Trp Ile Glu Glu Thr Ile Ala Ser His

260

265

270

5

<210> 36

<211> 509

<212> PRT

10 <213> Homo sapiens

<220>

<221> Dihydrolipoamide dehydrogenase, mitochondrial precursor

<222> (1)..(509)

<223> Accession No. as of 09 Dec 2002: P09622

15 <400> 36

Met Gln Ser Trp Ser Arg Val Tyr Cys Ser Leu Ala Lys Arg Gly His

1

5

10

15

Phe Asn Arg Ile Ser His Gly Leu Gln Gly Leu Ser Ala Val Pro Leu

20

20

25

30

Arg Thr Tyr Ala Asp Gln Pro Ile Asp Ala Asp Val Thr Val Ile Gly

35

40

45

Ser Gly Pro Gly Gly Tyr Val Ala Ala Ile Lys Ala Ala Gln Leu Gly

50

55

60

119/335

Phe Lys Thr Val Cys Ile Glu Lys Asn Glu Thr Leu Gly Gly Thr Cys
65 70 75 80
Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Leu Asn Asn Ser His
85 90 95
5 Tyr Tyr His Met Ala His Gly Thr Asp Phe Ala Ser Arg Gly Ile Glu
100 105 110
Met Ser Glu Val Arg Leu Asn Leu Asp Lys Met Met Glu Gln Lys Ser
115 120 125
Thr Ala Val Lys Ala Leu Thr Gly Gly Ile Ala His Leu Phe Lys Gln
10 130 135 140
Asn Lys Val Val His Val Asn Gly Tyr Gly Lys Ile Thr Gly Lys Asn
145 150 155 160
Gln Val Thr Ala Thr Lys Ala Asp Gly Gly Thr Gln Val Ile Asp Thr
165 170 175
15 Lys Asn Ile Leu Ile Ala Thr Gly Ser Glu Val Thr Pro Phe Pro Gly
180 185 190
Ile Thr Ile Asp Glu Asp Thr Ile Val Ser Ser Thr Gly Ala Leu Ser
195 200 205
Leu Lys Lys Val Pro Glu Lys Met Val Val Ile Gly Ala Gly Val Ile
20 210 215 220
Gly Val Glu Leu Gly Ser Val Trp Gln Arg Leu Gly Ala Asp Val Thr
225 230 235 240
Ala Val Glu Phe Leu Gly His Val Gly Gly Val Gly Ile Asp Met Glu
245 250 255

120/335

Ile Ser Lys Asn Phe Gln Arg Ile Leu Gln Lys Gln Gly Phe Lys Phe
260 265 270

Lys Leu Asn Thr Lys Val Thr Gly Ala Thr Lys Lys Ser Asp Gly Lys
275 280 285

5 Ile Asp Val Ser Ile Glu Ala Ala Ser Gly Gly Lys Ala Glu Val Ile
290 295 300

Thr Cys Asp Val Leu Leu Val Cys Ile Gly Arg Arg Pro Phe Thr Lys
305 310 315 320

Asn Leu Gly Leu Glu Glu Leu Gly Ile Glu Leu Asp Pro Arg Gly Arg
10 325 330 335

Ile Pro Val Asn Thr Arg Phe Gln Thr Lys Ile Pro Asn Ile Tyr Ala
340 345 350

Ile Gly Asp Val Val Ala Gly Pro Met Leu Ala His Lys Ala Glu Asp
355 360 365

15 Glu Gly Ile Ile Cys Val Glu Gly Met Ala Gly Gly Ala Val His Ile
370 375 380

Asp Tyr Asn Cys Val Pro Ser Val Ile Tyr Thr His Pro Glu Val Ala
385 390 395 400

Trp Val Gly Lys Ser Glu Glu Gln Leu Lys Glu Glu Gly Ile Glu Tyr
20 405 410 415

Lys Val Gly Lys Phe Pro Phe Ala Ala Asn Ser Arg Ala Lys Thr Asn
420 425 430

Ala Asp Thr Asp Gly Met Val Lys Ile Leu Gly Gln Lys Ser Thr Asp
435 440 445

121/335

Arg Val Leu Gly Ala His Ile Leu Gly Pro Gly Ala Gly Glu Met Val
450 455 460
Asn Glu Ala Ala Leu Ala Leu Glu Tyr Gly Ala Ser Cys Glu Asp Ile
465 470 475 480
5 Ala Arg Val Cys His Ala His Pro Thr Leu Ser Glu Ala Phe Arg Glu
485 490 495
Ala Asn Leu Ala Ala Ser Phe Gly Lys Ser Ile Asn Phe
500 505

10

<210> 37
<211> 290
<212> PRT
<213> Homo sapiens

15 <220>

<221> Enoyl-CoA hydratase, mitochondrial precursor
<222> (1)..(290)
<223> Accession No. as of 09 Dec 2002: P30084
<400> 37

20

Met Ala Ala Leu Arg Val Leu Leu Ser Cys Ala Arg Gly Pro Leu Arg
1 5 10 15
Pro Pro Val Arg Cys Pro Ala Trp Arg Pro Phe Ala Ser Gly Ala Asn
20 25 30

122/335

Phe Glu Tyr Ile Ile Ala Glu Lys Arg Gly Lys Asn Asn Thr Val Gly
35 40 45

Leu Ile Gln Leu Asn Arg Pro Lys Ala Leu Asn Ala Leu Cys Asp Gly
50 55 60

5 Leu Ile Asp Glu Leu Asn Gln Ala Leu Lys Ile Phe Glu Glu Asp Pro
65 70 75 80

Ala Val Gly Ala Ile Val Leu Thr Gly Gly Asp Lys Ala Phe Ala Ala
85 90 95

Gly Ala Asp Ile Lys Glu Met Gln Asn Leu Ser Phe Gln Asp Cys Tyr
10 100 105 110

Ser Ser Lys Phe Leu Lys His Trp Asp His Leu Thr Gln Val Lys Lys
115 120 125

Pro Val Ile Ala Ala Val Asn Gly Tyr Ala Phe Gly Gly Gly Cys Glu
130 135 140

15 Leu Ala Met Met Cys Asp Ile Ile Tyr Ala Gly Glu Lys Ala Gln Phe
145 150 155 160

Ala Gln Pro Glu Ile Leu Ile Gly Thr Ile Pro Gly Ala Gly Gly Thr
165 170 175

Gln Arg Leu Thr Arg Ala Val Gly Lys Ser Leu Ala Met Glu Met Val
20 180 185 190

Leu Thr Gly Asp Arg Ile Ser Ala Gln Asp Ala Lys Gln Ala Gly Leu
195 200 205

Val Ser Lys Ile Cys Pro Val Glu Thr Leu Val Glu Glu Ala Ile Gln
210 215 220

123/335

Cys Ala Glu Lys Ile Ala Ser Asn Ser Lys Ile Val Val Ala Met Ala

225

230

235

240

Lys Glu Ser Val Asn Ala Ala Phe Glu Met Thr Leu Thr Glu Gly Ser

245

250

255

5 Lys Leu Glu Lys Lys Leu Phe Tyr Ser Thr Phe Ala Thr Asp Asp Arg

260

265

270

Lys Glu Gly Met Thr Ala Phe Val Glu Lys Arg Lys Ala Asn Phe Lys

275

280

285

Asp Gln

10

290

<210> 38

<211> 160

15 <212> PRT

<213> Homo sapiens

<220>

<221> Heat-shock 20 kDa like-protein p20

<222> (1)..(160)

20 <223> Accession No. as of 09 Dec 2002: O14558

<400> 38

Met Glu Ile Pro Val Pro Val Gln Pro Ser Trp Leu Arg Arg Ala Ser

1

5

10

15

124/335

Ala Pro Leu Pro Gly Leu Ser Ala Pro Gly Arg Leu Phe Asp Gln Arg
20 25 30
Phe Gly Glu Gly Leu Leu Glu Ala Glu Leu Ala Ala Leu Cys Pro Thr
35 40 45
5 Thr Leu Ala Pro Tyr Tyr Leu Arg Ala Pro Ser Val Ala Leu Pro Val
50 55 60
Ala Gln Val Pro Thr Asp Pro Gly His Phe Ser Val Leu Leu Asp Val
65 70 75 80
Lys His Phe Ser Pro Glu Glu Ile Ala Val Lys Val Val Gly Glu His
10 85 90 95
Val Glu Val His Ala Arg His Glu Glu Arg Pro Asp Glu His Gly Phe
100 105 110
Val Ala Arg Glu Phe His Arg Arg Tyr Arg Leu Pro Pro Gly Val Asp
115 120 125
15 Pro Ala Ala Val Thr Ser Ala Leu Ser Pro Glu Gly Val Leu Ser Ile
130 135 140
Gln Ala Ala Pro Ala Ser Ala Gln Ala Pro Pro Pro Ala Ala Ala Lys
145 150 155 160

20

<210> 39

<211> 151

<212> PRT

<213> Homo sapiens

125/335

<220>

<221> Myosin light chain alkali, non-muscle isoform

<222> (1)..(151)

<223> Accession No. as of 09 Dec 2002: P16475

5 <400> 39

Met Cys Asp Phe Thr Glu Asp Gln Thr Ala Glu Phe Lys Glu Ala Phe
1 5 10 15
Gln Leu Phe Asp Arg Thr Gly Asp Gly Lys Ile Leu Tyr Ser Gln Cys
10 20 25 30
Gly Asp Val Met Arg Ala Leu Gly Gln Asn Pro Thr Asn Ala Glu Val
35 40 45
Leu Lys Val Leu Gly Asn Pro Lys Ser Asp Glu Met Asn Val Lys Val
50 55 60
15 Leu Asp Phe Glu His Phe Leu Pro Met Leu Gln Thr Val Ala Lys Asn
65 70 75 80
Lys Asp Gln Gly Thr Tyr Glu Asp Tyr Val Glu Gly Leu Arg Val Phe
85 90 95
Asp Lys Glu Gly Asn Gly Thr Val Met Gly Ala Glu Ile Arg His Val
20 100 105 110
Leu Val Thr Leu Gly Glu Lys Met Thr Glu Glu Glu Val Glu Met Leu
115 120 125
Val Ala Gly His Glu Asp Ser Asn Gly Cys Ile Asn Tyr Glu Ala Phe
130 135 140

Val Arg His Ile Leu Ser Gly

145

150

5 <210> 40

<211> 592

<212> PRT

<213> Homo sapiens

<220>

10 <221> Calnexin precursor

<222> (1)..(592)

<223> Accession No. as of 09 Dec 2002: P27824

<400> 40

15 Met Glu Gly Lys Trp Leu Leu Cys Met Leu Leu Val Leu Gly Thr Ala

1

5

10

15

Ile Val Glu Ala His Asp Gly His Asp Asp Asp Val Ile Asp Ile Glu

20

25

30

Asp Asp Leu Asp Asp Val Ile Glu Glu Val Glu Asp Ser Lys Pro Asp

20

35

40

45

Thr Thr Ala Pro Pro Ser Ser Pro Lys Val Thr Tyr Lys Ala Pro Val

50

55

60

Pro Thr Gly Glu Val Tyr Phe Ala Asp Ser Phe Asp Arg Gly Thr Leu

65

70

75

80

127/335

Ser Gly Trp Ile Leu Ser Lys Ala Lys Lys Asp Asp Thr Asp Asp Glu
85 90 95

Ile Ala Lys Tyr Asp Gly Lys Trp Glu Val Glu Glu Met Lys Glu Ser
100 105 110

5 Lys Leu Pro Gly Asp Lys Gly Leu Val Leu Met Ser Arg Ala Lys His
115 120 125

His Ala Ile Ser Ala Lys Leu Asn Lys Pro Phe Leu Phe Asp Thr Lys
130 135 140

Pro Leu Ile Val Gln Tyr Glu Val Asn Phe Gln Asn Gly Ile Glu Cys
10 145 150 155 160

Gly Gly Ala Tyr Val Lys Leu Leu Ser Lys Thr Pro Glu Leu Asn Leu
165 170 175

Asp Gln Phe His Asp Lys Thr Pro Tyr Thr Ile Met Phe Gly Pro Asp
180 185 190

15 Lys Cys Gly Glu Asp Tyr Lys Leu His Phe Ile Phe Arg His Lys Asn
195 200 205

Pro Lys Thr Gly Ile Tyr Glu Glu Lys His Ala Lys Arg Pro Asp Ala
210 215 220

Asp Leu Lys Thr Tyr Phe Thr Asp Lys Lys Thr His Leu Tyr Thr Leu
20 225 230 235 240

Ile Leu Asn Pro Asp Asn Ser Phe Glu Ile Leu Val Asp Gln Ser Val
245 250 255

Val Asn Ser Gly Asn Leu Leu Asn Asp Met Thr Pro Pro Val Asn Pro
260 265 270

Ser Arg Glu Ile Glu Asp Pro Glu Asp Arg Lys Pro Glu Asp Trp Asp
275 280 285

Glu Arg Pro Lys Ile Pro Asp Pro Glu Ala Val Lys Pro Asp Asp Trp
290 295 300

5 Asp Glu Asp Ala Pro Ala Lys Ile Pro Asp Glu Glu Ala Thr Lys Pro
305 310 315 320

Glu Gly Trp Leu Asp Asp Glu Pro Glu Tyr Val Pro Asp Pro Asp Ala
325 330 335

Glu Lys Pro Glu Asp Trp Asp Glu Asp Met Asp Gly Glu Trp Glu Ala
10 340 345 350

Pro Gln Ile Ala Asn Pro Arg Cys Glu Ser Ala Pro Gly Cys Gly Val
355 360 365

Trp Gln Arg Pro Val Ile Asp Asn Pro Asn Tyr Lys Gly Lys Trp Lys
370 375 380

15 Pro Pro Met Ile Asp Asn Pro Ser Tyr Gln Gly Ile Trp Lys Pro Arg
385 390 395 400

Lys Ile Pro Asn Pro Asp Phe Phe Glu Asp Leu Glu Pro Phe Arg Met
405 410 415

Thr Pro Phe Ser Ala Ile Gly Leu Glu Leu Trp Ser Met Thr Ser Asp
20 420 425 430

Ile Phe Phe Asp Asn Phe Ile Ile Cys Ala Asp Arg Arg Ile Val Asp
435 440 445

Asp Trp Ala Asn Asp Gly Trp Gly Leu Lys Lys Ala Ala Asp Gly Ala
450 455 460

129/335

Ala Glu Pro Gly Val Val Gly Gln Met Ile Glu Ala Ala Glu Glu Arg
465 470 475 480
Pro Trp Leu Trp Val Val Tyr Ile Leu Thr Val Ala Leu Pro Val Phe
485 490 495
5 Leu Val Ile Leu Phe Cys Cys Ser Gly Lys Lys Gln Thr Ser Gly Met
500 505 510
Glu Tyr Lys Lys Thr Asp Ala Pro Gln Pro Asp Val Lys Glu Glu Glu
515 520 525
Glu Glu Lys Glu Glu Glu Lys Asp Lys Gly Asp Glu Glu Glu Glu Gly
10 530 535 540
Glu Glu Lys Leu Glu Glu Lys Gln Lys Ser Asp Ala Glu Glu Asp Gly
545 550 555 560
Gly Thr Val Ser Gln Glu Glu Glu Asp Arg Lys Pro Lys Ala Glu Glu
565 570 575
15 Asp Glu Ile Leu Asn Arg Ser Pro Arg Asn Arg Lys Pro Arg Arg Glu
580 585 590

<210> 41

20 <211> 282

<212> PRT

<213> Homo sapiens

<220>

<221> Complement component 1

130/335

<222> (1)..(282)

<223> Accession No. as of 09 Dec 2002: Q07021

<400> 41

5 Met Leu Pro Leu Leu Arg Cys Val Pro Arg Val Leu Gly Ser Ser Val
1 5 10 15
Ala Gly Leu Arg Ala Ala Ala Pro Ala Ser Pro Phe Arg Gln Leu Leu
20 25 30
Gln Pro Ala Pro Arg Leu Cys Thr Arg Pro Phe Gly Leu Leu Ser Val
10 35 40 45
Arg Ala Gly Ser Glu Arg Arg Pro Gly Leu Leu Arg Pro Arg Gly Pro
50 55 60
Cys Ala Cys Gly Cys Gly Cys Gly Ser Leu His Thr Asp Gly Asp Lys
65 70 75 80
15 Ala Phe Val Asp Phe Leu Ser Asp Glu Ile Lys Glu Glu Arg Lys Ile
85 90 95
Gln Lys His Lys Thr Leu Pro Lys Met Ser Gly Gly Trp Glu Leu Glu
100 105 110
Leu Asn Gly Thr Glu Ala Lys Leu Val Arg Lys Val Ala Gly Glu Lys
20 115 120 125
Ile Thr Val Thr Phe Asn Ile Asn Asn Ser Ile Pro Pro Thr Phe Asp
130 135 140
Gly Glu Glu Glu Pro Ser Gln Gly Gln Lys Val Glu Glu Gln Glu Pro
145 150 155 160

Glu Leu Thr Ser Thr Pro Asn Phe Val Val Glu Val Ile Lys Asn Asp
165 170 175
Asp Gly Lys Lys Ala Leu Val Leu Asp Cys His Tyr Pro Glu Asp Glu
180 185 190
5 Val Gly Gln Glu Asp Glu Ala Glu Ser Asp Ile Phe Ser Ile Arg Glu
195 200 205
Val Ser Phe Gln Ser Thr Gly Glu Ser Glu Trp Lys Asp Thr Asn Tyr
210 215 220
Thr Leu Asn Thr Asp Ser Leu Asp Trp Ala Leu Tyr Asp His Leu Met
10 225 230 235 240
Asp Phe Leu Ala Asp Arg Gly Val Asp Asn Thr Phe Ala Asp Glu Leu
245 250 255
Val Glu Leu Ser Thr Ala Leu Glu His Gln Glu Tyr Ile Thr Phe Leu
260 265 270
15 Glu Asp Leu Lys Ser Phe Val Lys Ser Gln
275 280

<210> 42

20 <211> 727

<212> PRT

<213> Homo sapiens

<220>

<221> NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

precursor

<222> (1)..(727)

<223> Accession No. as of 09 Dec 2002: P28331

<400> 42

5

Met Leu Arg Ile Pro Val Arg Arg Ala Leu Val Gly Leu Ser Lys Ser

1 5 10 15

Pro Lys Gly Cys Val Arg Thr Thr Ala Thr Ala Ala Ser Asn Leu Ile

20 25 30

10 Glu Val Phe Val Asp Gly Gln Ser Val Met Val Glu Pro Gly Thr Thr

35 40 45

Val Leu Gln Ala Cys Glu Lys Val Gly Met Gln Ile Pro Arg Phe Cys

50 55 60

Tyr His Glu Arg Leu Ser Val Ala Gly Asn Cys Arg Met Cys Leu Val

15 65 70 75 80

Glu Ile Glu Lys Ala Pro Lys Val Val Ala Ala Cys Ala Met Pro Val

85 90 95

Met Lys Gly Trp Asn Ile Leu Thr Asn Ser Glu Lys Ser Lys Lys Ala

100 105 110

20 Arg Glu Gly Val Met Glu Phe Leu Leu Ala Asn His Pro Leu Asp Cys

115 120 125

Pro Ile Cys Asp Gln Gly Gly Glu Cys Asp Leu Gln Asp Gln Ser Met

130 135 140

Met Phe Gly Asn Asp Arg Ser Arg Phe Leu Glu Gly Lys Arg Ala Val

133/335

145 150 155 160
Glu Asp Lys Asn Ile Gly Pro Leu Val Lys Thr Ile Met Thr Arg Cys
 165 170 175
Ile Gln Cys Thr Arg Cys Ile Arg Phe Ala Ser Glu Ile Ala Gly Val
5 180 185 190
Asp Asp Leu Gly Thr Thr Gly Arg Gly Asn Asp Met Gln Val Gly Thr
 195 200 205
Tyr Ile Glu Lys Met Phe Met Ser Glu Leu Ser Gly Asn Ile Ile Asp
 210 215 220
10 Ile Cys Pro Val Gly Ala Leu Thr Ser Lys Pro Tyr Ala Phe Thr Ala
 225 230 235 240
Arg Pro Trp Glu Thr Arg Lys Thr Glu Ser Ile Asp Val Met Asp Ala
 245 250 255
Val Gly Ser Asn Ile Val Val Ser Thr Arg Thr Gly Glu Val Met Arg
15 260 265 270
Ile Leu Pro Arg Met His Glu Asp Ile Asn Glu Glu Trp Ile Ser Asp
 275 280 285
Lys Thr Arg Phe Ala Tyr Asp Gly Leu Lys Arg Gln Arg Leu Thr Glu
 290 295 300
20 Pro Met Val Arg Asn Glu Lys Gly Leu Leu Thr Tyr Thr Ser Trp Glu
 305 310 315 320
Asp Ala Leu Ser Arg Val Ala Gly Met Leu Gln Ser Phe Gln Gly Lys
 325 330 335
Asp Val Ala Ala Ile Ala Gly Gly Leu Val Asp Ala Glu Ala Leu Val

134/335

340 345 350
Ala Leu Lys Asp Leu Leu Asn Arg Val Asp Ser Asp Thr Leu Cys Thr
355 360 365
Glu Glu Val Phe Pro Thr Ala Gly Ala Gly Thr Asp Leu Arg Ser Asn
5 370 375 380
Tyr Leu Leu Asn Thr Thr Ile Ala Gly Val Glu Glu Ala Asp Val Val
385 390 395 400
Leu Leu Val Gly Thr Asn Pro Arg Phe Glu Ala Pro Leu Phe Asn Ala
405 410 415
10 Trp Ile Arg Lys Ser Trp Leu His Asn Asp Leu Lys Val Ala Leu Ile
420 425 430
Gly Ser Pro Val Asp Leu Thr Tyr Thr Tyr Asp His Leu Gly Asp Ser
435 440 445
Pro Lys Ile Leu Gln Asp Ile Ala Ser Gly Ser His Pro Phe Ser Gln
15 450 455 460
Val Leu Lys Glu Ala Lys Lys Pro Met Val Val Leu Gly Ser Ser Ala
465 470 475 480
Leu Gln Arg Asn Asp Gly Ala Ala Ile Leu Ala Ala Val Ser Ser Ile
485 490 495
20 Ala Gln Lys Ile Arg Met Thr Ser Gly Val Thr Gly Asp Trp Lys Val
500 505 510
Met Asn Ile Leu His Arg Ile Ala Ser Gln Val Ala Ala Leu Asp Leu
515 520 525
Gly Tyr Lys Pro Gly Val Glu Ala Ile Arg Lys Asn Pro Pro Lys Val

135/335

530 535 540
Leu Phe Leu Leu Gly Ala Asp Gly Gly Cys Ile Thr Arg Gln Asp Leu
545 550 555 560
Pro Lys Asp Cys Phe Ile Ile Tyr Gln Gly His His Gly Asp Val Gly
5 565 570 575
Ala Pro Ile Ala Asp Val Ile Leu Pro Gly Ala Ala Tyr Thr Glu Lys
580 585 590
Ser Ala Thr Tyr Val Asn Thr Glu Gly Arg Ala Gln Gln Thr Lys Val
595 600 605
10 Ala Val Thr Pro Pro Gly Leu Ala Arg Glu Asp Trp Lys Ile Ile Arg
610 615 620
Ala Leu Ser Glu Ile Ala Gly Met Thr Leu Pro Tyr Asp Thr Leu Asp
625 630 635 640
Gln Val Arg Asn Arg Leu Glu Glu Phe Ser Pro Asn Leu Val Arg Tyr
15 645 650 655
Asp Asp Ile Glu Gly Ala Asn Tyr Phe Gln Gln Ala Asn Glu Leu Ser
660 665 670
Lys Leu Val Asn Gln Gln Leu Leu Ala Asp Pro Leu Val Pro Pro Gln
675 680 685
20 Leu Thr Leu Lys Asp Phe Tyr Met Thr Asp Ser Ile Ser Arg Ala Ser
690 695 700
Gln Thr Met Ala Lys Cys Val Lys Ala Val Thr Glu Gly Ala Gln Ala
705 710 715 720
Val Glu Glu Pro Ser Ile Cys

725

<210> 43

5 <211> 491

<212> PRT

<213> Homo sapiens

<220>

<221> Pre-B cell enhancing factor precursor

10 <222> (1)..(491)

<223> Accession No. as of 09 Dec 2002: P43490

<400> 43

Met Asn Pro Ala Ala Glu Ala Glu Phe Asn Ile Leu Leu Ala Thr Asp

15 1 5 10 15

Ser Tyr Lys Val Thr His Tyr Lys Gln Tyr Pro Pro Asn Thr Ser Lys

20 25 30

Val Tyr Ser Tyr Phe Glu Cys Arg Glu Lys Lys Thr Glu Asn Ser Lys

35 40 45

20 Leu Arg Lys Val Lys Tyr Glu Glu Thr Val Phe Tyr Gly Leu Gln Tyr

50 55 60

Ile Leu Asn Lys Tyr Leu Lys Gly Lys Val Val Thr Lys Glu Lys Ile

65 70 75 80

Gln Glu Ala Lys Asp Val Tyr Lys Glu His Phe Gln Asp Asp Val Phe

137/335

	85	90	95
	Asn Glu Lys Gly Trp Asn Tyr Ile Leu Glu Lys Tyr Asp Gly His Leu		
	100	105	110
	Pro Ile Glu Ile Lys Ala Val Pro Glu Gly Phe Val Ile Pro Arg Gly		
5	115	120	125
	Asn Val Leu Phe Thr Val Glu Asn Thr Asp Pro Glu Cys Tyr Trp Leu		
	130	135	140
	Thr Asn Trp Ile Glu Thr Ile Leu Val Gln Ser Trp Tyr Pro Ile Thr		
	145	150	155
			160
10	Val Ala Thr Asn Ser Arg Glu Gln Lys Lys Ile Leu Ala Lys Tyr Leu		
	165	170	175
	Leu Glu Thr Ser Gly Asn Leu Asp Gly Leu Glu Tyr Lys Leu His Asp		
	180	185	190
	Phe Gly Tyr Arg Gly Val Ser Ser Gln Glu Thr Ala Gly Ile Gly Ala		
15	195	200	205
	Ser Ala His Leu Val Asn Phe Lys Gly Thr Asp Thr Val Ala Gly Leu		
	210	215	220
	Ala Leu Ile Lys Lys Tyr Tyr Gly Thr Lys Asp Pro Val Pro Gly Tyr		
	225	230	235
			240
20	Ser Val Pro Ala Ala Glu His Ser Thr Ile Thr Ala Trp Gly Lys Asp		
	245	250	255
	His Glu Lys Asp Ala Phe Glu His Ile Val Thr Gln Phe Ser Ser Val		
	260	265	270
	Pro Val Ser Val Val Ser Asp Ser Tyr Asp Ile Tyr Asn Ala Cys Glu		

138/335

275 280 285
Lys Ile Trp Gly Glu Asp Leu Arg His Leu Ile Val Ser Arg Ser Thr
290 295 300
Gln Ala Pro Leu Ile Ile Arg Pro Asp Ser Gly Asn Pro Leu Asp Thr
5 305 310 315 320
Val Leu Lys Val Leu Glu Ile Leu Gly Lys Lys Phe Pro Val Thr Glu
325 330 335
Asn Ser Lys Gly Tyr Lys Leu Leu Pro Pro Tyr Leu Arg Val Ile Gln
340 345 350
10 Gly Asp Gly Val Asp Ile Asn Thr Leu Gln Glu Ile Val Glu Gly Met
355 360 365
Lys Gln Lys Met Trp Ser Ile Glu Asn Ile Ala Phe Gly Ser Gly Gly
370 375 380
Gly Leu Leu Gln Lys Leu Thr Arg Asp Leu Leu Asn Cys Ser Phe Lys
15 385 390 395 400
Cys Ser Tyr Val Val Thr Asn Gly Leu Gly Ile Asn Val Phe Lys Asp
405 410 415
Pro Val Ala Asp Pro Asn Lys Arg Ser Lys Lys Gly Arg Leu Ser Leu
420 425 430
20 His Arg Thr Pro Ala Gly Asn Phe Val Thr Leu Glu Glu Gly Lys Gly
435 440 445
Asp Leu Glu Glu Tyr Gly Gln Asp Leu Leu His Thr Val Phe Lys Asn
450 455 460
Gly Lys Val Thr Lys Ser Tyr Ser Phe Asp Glu Ile Arg Lys Asn Ala

139/335

465 470 475 480

Gln Leu Asn Ile Glu Leu Glu Ala Ala His His

485 490

5

<210> 44

<211> 135

<212> PRT

<213> Homo sapiens

10 <220>

<221> Retinol-binding protein I, cellular

<222> (1)..(135)

<223> Accession No. as of 09 Dec 2002: P09455

<400> 44

15

Met Pro Val Asp Phe Thr Gly Tyr Trp Lys Met Leu Val Asn Glu Asn

1 5 10 15

Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys

20 25 30

20 Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp

35 40 45

His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp

50 55 60

Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp

140/335

65 70 75 80
Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys
 85 90 95
Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu
5 100 105 110
Gly Asp Glu Leu His Leu Glu Met Arg Val Glu Gly Val Val Cys Lys
 115 120 125
Gln Val Phe Lys Lys Val Gln
 130 135

10

<210> 45
<211> 544
<212> PRT
15 <213> Homo sapiens
<220>
<221> T-complex protein 1, gamma subunit
<222> (1) .. (544)
<223> Accession No. as of 09 Dec 2002: P49368
20 <400> 45

Met Gly His Arg Pro Val Leu Val Leu Ser Gln Asn Thr Lys Arg Glu
1 5 10 15
Ser Gly Arg Lys Val Gln Ser Gly Asn Ile Asn Ala Ala Lys Thr Ile

141/335

20 25 30
Ala Asp Ile Ile Arg Thr Cys Leu Gly Pro Lys Ser Met Met Lys Met
35 40 45
Leu Leu Asp Pro Met Gly Gly Ile Val Met Thr Asn Asp Gly Asn Ala
5 50 55 60
Ile Leu Arg Glu Ile Gln Val Gln His Pro Ala Ala Lys Ser Met Ile
65 70 75 80
Glu Ile Ser Arg Thr Gln Asp Glu Glu Val Gly Asp Gly Thr Thr Ser
85 90 95
10 Val Ile Ile Leu Ala Gly Glu Met Leu Ser Val Ala Glu His Phe Leu
100 105 110
Glu Gln Gln Met His Pro Thr Val Val Ile Ser Ala Tyr Arg Lys Ala
115 120 125
Leu Asp Asp Met Ile Ser Thr Leu Lys Lys Ile Ser Ile Pro Val Asp
15 130 135 140
Ile Ser Asp Ser Asp Met Met Leu Asn Ile Ile Asn Ser Ser Ile Thr
145 150 155 160
Thr Lys Ala Ile Ser Arg Trp Ser Ser Leu Ala Cys Asn Ile Ala Leu
165 170 175
20 Asp Ala Val Lys Met Val Gln Phe Glu Glu Asn Gly Arg Lys Glu Ile
180 185 190
Asp Ile Lys Lys Tyr Ala Arg Val Glu Lys Ile Pro Gly Gly Ile Ile
195 200 205
Glu Asp Ser Cys Val Leu Arg Gly Val Met Ile Asn Lys Asp Val Thr

210 215 220
His Pro Arg Met Arg Arg Tyr Ile Lys Asn Pro Arg Ile Val Leu Leu
225 230 235 240
Asp Ser Ser Leu Glu Tyr Lys Lys Gly Glu Ser Gln Thr Asp Ile Glu
5 245 250 255
Ile Thr Arg Glu Glu Asp Phe Thr Arg Ile Leu Gln Met Glu Glu Glu
260 265 270
Tyr Ile Gln Gln Leu Cys Glu Asp Ile Ile Gln Leu Lys Pro Asp Val
275 280 285
10 Val Ile Thr Glu Lys Gly Ile Ser Asp Leu Ala Gln His Tyr Leu Met
290 295 300
Arg Ala Asn Ile Thr Ala Ile Arg Arg Val Arg Lys Thr Asp Asn Asn
305 310 315 320
Arg Ile Ala Arg Ala Cys Gly Ala Arg Ile Val Ser Arg Pro Glu Glu
15 325 330 335
Leu Arg Glu Asp Asp Val Gly Thr Gly Ala Gly Leu Leu Glu Ile Lys
340 345 350
Lys Ile Gly Asp Glu Tyr Phe Thr Phe Ile Thr Asp Cys Lys Asp Pro
355 360 365
20 Lys Ala Cys Thr Ile Leu Leu Arg Gly Ala Ser Lys Glu Ile Leu Ser
370 375 380
Glu Val Glu Arg Asn Leu Gln Asp Ala Met Gln Val Cys Arg Asn Val
385 390 395 400
Leu Leu Asp Pro Gln Leu Val Pro Gly Gly Gly Ala Ser Glu Met Ala

143/335

405 410 415
Val Ala His Ala Leu Thr Glu Lys Ser Lys Ala Met Thr Gly Val Glu
420 425 430
Gln Trp Pro Tyr Arg Ala Val Ala Gln Ala Leu Glu Val Ile Pro Arg
5 435 440 445
Thr Leu Ile Gln Asn Cys Gly Ala Ser Thr Ile Arg Leu Leu Thr Ser
450 455 460
Leu Arg Ala Lys His Thr Gln Glu Asn Cys Glu Thr Trp Gly Val Asn
465 470 475 480
10 Gly Glu Thr Gly Thr Leu Val Asp Met Lys Glu Leu Gly Ile Trp Glu
485 490 495
Pro Leu Ala Val Lys Leu Gln Thr Tyr Lys Thr Ala Val Glu Thr Ala
500 505 510
Val Leu Leu Leu Arg Ile Asp Asp Ile Val Ser Gly His Lys Lys Lys
15 515 520 525
Gly Asp Asp Gln Ser Arg Gln Gly Gly Ala Pro Asp Ala Gly Gln Glu
530 535 540

20 <210> 46

<211> 461

<212> PRT

<213> Homo sapiens

<220>

<221> Placental ribonuclease inhibitor

<222> (1)..(461)

<223> Accession No. as of 09 Dec 2002: P13489

<400> 46

5

Met Ser Leu Asp Ile Gln Ser Leu Asp Ile Gln Cys Glu Glu Leu Ser

1 5 10 15

Asp Ala Arg Trp Ala Glu Leu Leu Pro Leu Leu Gln Gln Cys Gln Val

20 25 30

10 Val Arg Leu Asp Asp Cys Gly Leu Thr Glu Ala Arg Cys Lys Asp Ile

35 40 45

Ser Ser Ala Leu Arg Val Asn Pro Ala Leu Ala Glu Leu Asn Leu Arg

50 55 60

Ser Asn Glu Leu Gly Asp Val Gly Val His Cys Val Leu Gln Gly Leu

15 65 70 75 80

Gln Thr Pro Ser Cys Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Cys

85 90 95

Leu Thr Gly Ala Gly Cys Gly Val Leu Ser Ser Thr Leu Arg Thr Leu

100 105 110

20 Pro Thr Leu Gln Glu Leu His Leu Ser Asp Asn Leu Leu Gly Asp Ala

115 120 125

Gly Leu Gln Leu Leu Cys Glu Gly Leu Leu Asp Pro Gln Cys Arg Leu

130 135 140

Glu Lys Leu Gln Leu Glu Tyr Cys Ser Leu Ser Ala Ala Ser Cys Glu

145/335

145 150 155 160
Pro Leu Ala Ser Val Leu Arg Ala Lys Pro Asp Phe Lys Glu Leu Thr
 165 170 175
Val Ser Asn Asn Asp Ile Asn Glu Ala Gly Val Arg Val Leu Cys Gln
5 180 185 190
Gly Leu Lys Asp Ser Pro Cys Gln Leu Glu Ala Leu Lys Leu Glu Ser
 195 200 205
Cys Gly Val Thr Ser Asp Asn Cys Arg Asp Leu Cys Gly Ile Val Ala
 210 215 220
10 Ser Lys Ala Ser Leu Arg Glu Leu Ala Leu Gly Ser Asn Lys Leu Gly
225 230 235 240
Asp Val Gly Met Ala Glu Leu Cys Pro Gly Leu Leu His Pro Ser Ser
 245 250 255
Arg Leu Arg Thr Leu Trp Ile Trp Glu Cys Gly Ile Thr Ala Lys Gly
15 260 265 270
Cys Gly Asp Leu Cys Arg Val Leu Arg Ala Lys Glu Ser Leu Lys Glu
 275 280 285
Leu Ser Leu Ala Gly Asn Glu Leu Gly Asp Glu Gly Ala Arg Leu Leu
 290 295 300
20 Cys Glu Thr Leu Leu Glu Pro Gly Cys Gln Leu Glu Ser Leu Trp Val
305 310 315 320
Lys Ser Cys Ser Phe Thr Ala Ala Cys Cys Ser His Phe Ser Ser Val
 325 330 335
Leu Ala Gln Asn Arg Phe Leu Leu Glu Leu Gln Ile Ser Asn Asn Arg

146/335

340 345 350
Leu Glu Asp Ala Gly Val Arg Glu Leu Cys Gln Gly Leu Gly Gln Pro
355 360 365
Gly Ser Val Leu Arg Val Leu Trp Leu Ala Asp Cys Asp Val Ser Asp
5 370 375 380
Ser Ser Cys Ser Ser Leu Ala Ala Thr Leu Leu Ala Asn His Ser Leu
385 390 395 400
Arg Glu Leu Asp Leu Ser Asn Asn Cys Leu Gly Asp Ala Gly Ile Leu
405 410 415
10 Gln Leu Val Glu Ser Val Arg Gln Pro Gly Cys Leu Leu Glu Gln Leu
420 425 430
Val Leu Tyr Asp Ile Tyr Trp Ser Glu Glu Met Glu Asp Arg Leu Gln
435 440 445
Ala Leu Glu Lys Asp Lys Pro Ser Leu Arg Val Ile Ser
15 450 455 460

<210> 47
<211> 317
20 <212> PRT
<213> Homo sapiens
<220>
<221> Guanine nucleotide-binding protein beta subunit-like protein
12.3

<222> (1)..(317)

<223> Accession No. as of 09 Dec 2002: P25388

<400> 47

5 Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly
1 5 10 15
Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu
20 25 30
Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp
10 35 40 45
Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His
50 55 60
Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser
65 70 75 80
15 Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr
85 90 95
Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
100 105 110
Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr
20 115 120 125
Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp
130 135 140
Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser
145 150 155 160

Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val
165 170 175

Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr
180 185 190

5 Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala
195 200 205

Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly
210 215 220

Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
10 225 230 235 240

Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
245 250 255

Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln
260 265 270

15 Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser
275 280 285

Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp
290 295 300

Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg
20 305 310 315

<210> 48

<211> 172

<212> PRT

<213> Homo sapiens

<220>

<221> Myosin regulatory light chain 2

5 <222> (1)..(172)

<223> Accession No. as of 10 Dec 2002: P24844

<400> 48

Met Ser Ser Lys Arg Ala Lys Ala Lys Thr Thr Lys Lys Arg Pro Gln
10 1 5 10 15
Arg Ala Thr Ser Asn Val Phe Ala Met Phe Asp Gln Ser Gln Ile Gln
20 25 30
Glu Phe Lys Glu Ala Phe Asn Met Ile Asp Gln Asn Arg Asp Gly Phe
35 40 45
15 Ile Asp Lys Glu Asp Leu His Asp Met Leu Ala Ser Leu Gly Lys Asn
50 55 60
Pro Thr Asp Glu Tyr Leu Glu Gly Met Met Ser Glu Ala Pro Gly Pro
65 70 75 80
Ile Asn Phe Thr Met Phe Leu Thr Met Phe Gly Glu Lys Leu Asn Gly
20 85 90 95
Thr Asp Pro Glu Asp Val Ile Arg Asn Ala Phe Ala Cys Phe Asp Glu
100 105 110
Glu Ala Ser Gly Phe Ile His Glu Asp His Leu Arg Glu Leu Leu Thr
115 120 125

150/335

Thr Met Gly Asp Arg Phe Thr Asp Glu Glu Val Asp Glu Met Tyr Arg

130

135

140

Glu Ala Pro Ile Asp Lys Lys Gly Asn Phe Asn Tyr Val Glu Phe Thr

145

150

155

160

5 Arg Ile Leu Lys His Gly Ala Lys Asp Lys Asp Asp

165

170

<210> 49

10 <211> 114

<212> PRT

<213> Homo sapiens

<220>

<221> Calgranulin B

15 <222> (1)..(114)

<223> Accession No. as of 10 Dec 2002: P06702

<400> 49

Met Thr Cys Lys Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile

20 1

5

10

15

Asn Thr Phe His Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu

20

25

30

Asn Gln Gly Glu Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe

35

40

45

151/335

Leu Lys Lys Glu Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu

50

55

60

Asp Leu Asp Thr Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile

65

70

75

80

5 Met Leu Met Ala Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu

85

90

95

Gly Asp Glu Gly Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly

100

105

110

Thr Pro

10

<210> 50

<211> 348

15 <212> PRT

<213> Homo sapiens

<220>

<221> Macrophage capping protein

<222> (1)..(348)

20 <223> Accession No. as of 10 Dec 2002: P40121

<400> 50

Met Tyr Thr Ala Ile Pro Gln Ser Gly Ser Pro Phe Pro Gly Ser Val

1

5

10

15

152/335

Gln Asp Pro Gly Leu His Val Trp Arg Val Glu Lys Leu Lys Pro Val
20 25 30

Pro Val Ala Gln Glu Asn Gln Gly Val Phe Phe Ser Gly Asp Ser Tyr
35 40 45

5 Leu Val Leu His Asn Gly Pro Glu Glu Val Ser His Leu His Leu Trp
50 55 60

Ile Gly Gln Gln Ser Ser Arg Asp Glu Gln Gly Ala Cys Ala Val Leu
65 70 75 80

Ala Val His Leu Asn Thr Leu Leu Gly Glu Arg Pro Val Gln His Arg
10 85 90 95

Glu Val Gln Gly Asn Glu Ser Asp Leu Phe Met Ser Tyr Phe Pro Arg
100 105 110

Gly Leu Lys Tyr Gln Glu Gly Gly Val Glu Ser Ala Phe His Lys Thr
115 120 125

15 Ser Thr Gly Ala Pro Ala Ala Ile Lys Lys Leu Tyr Gln Val Lys Gly
130 135 140

Lys Lys Asn Ile Arg Ala Thr Glu Arg Ala Leu Asn Trp Asp Ser Phe
145 150 155 160

Asn Thr Gly Asp Cys Phe Ile Leu Asp Leu Gly Gln Asn Ile Phe Ala
20 165 170 175

Trp Cys Gly Gly Lys Ser Asn Ile Leu Glu Arg Asn Lys Ala Arg Asp
180 185 190

Leu Ala Leu Ala Ile Arg Asp Ser Glu Arg Gln Gly Lys Ala Gln Val
195 200 205

153/335

Glu Ile Val Thr Asp Gly Glu Glu Pro Ala Glu Met Ile Gln Val Leu
210 215 220
Gly Pro Lys Pro Ala Leu Lys Glu Gly Asn Pro Glu Glu Asp Leu Thr
225 230 235 240
5 Ala Asp Lys Ala Asn Ala Gln Ala Ala Ala Leu Tyr Lys Val Ser Asp
245 250 255
Ala Thr Gly Gln Met Asn Leu Thr Lys Val Ala Asp Ser Ser Pro Phe
260 265 270
Ala Leu Glu Leu Leu Ile Ser Asp Asp Cys Phe Val Leu Asp Asn Gly
10 275 280 285
Leu Cys Gly Lys Ile Tyr Ile Trp Lys Gly Arg Lys Ala Asn Glu Lys
290 295 300
Glu Arg Gln Ala Ala Leu Gln Val Ala Glu Gly Phe Ile Ser Arg Met
305 310 315 320
15 Gln Tyr Ala Pro Asn Thr Gln Val Glu Ile Leu Pro Gln Gly Arg Glu
325 330 335
Ser Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Lys
340 345

20

<210> 51

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<221> Annexin I

<222> (1)..(346)

<223> Accession No. as of 10 Dec 2002: P04083

5 <400> 51

Met Ala Met Val Ser Glu Phe Leu Lys Gln Ala Trp Phe Ile Glu Asn
1 5 10 15
Glu Glu Gln Glu Tyr Val Gln Thr Val Lys Ser Ser Lys Gly Gly Pro
10 20 25 30
Gly Ser Ala Val Ser Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val
35 40 45
Ala Ala Leu His Lys Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr
50 55 60
15 Ile Ile Asp Ile Leu Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile
65 70 75 80
Lys Ala Ala Tyr Leu Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu
85 90 95
Lys Lys Ala Leu Thr Gly His Leu Glu Glu Val Val Leu Ala Leu Leu
20 100 105 110
Lys Thr Pro Ala Gln Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys
115 120 125
Gly Leu Gly Thr Asp Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg
130 135 140

Thr Asn Lys Glu Ile Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu
145 150 155 160
Lys Arg Asp Leu Ala Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe
165 170 175
5 Arg Asn Ala Leu Leu Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe
180 185 190
Gly Val Asn Glu Asp Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu
195 200 205
Ala Gly Glu Arg Arg Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile
10 210 215 220
Leu Thr Thr Arg Ser Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr
225 230 235 240
Thr Lys Tyr Ser Lys His Asp Met Asn Lys Val Leu Asp Leu Glu Leu
245 250 255
15 Lys Gly Asp Ile Glu Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr
260 265 270
Ser Lys Pro Ala Phe Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly
275 280 285
Val Gly Thr Arg His Lys Ala Leu Ile Arg Ile Met Val Ser Arg Ser
20 290 295 300
Glu Ile Asp Met Asn Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly
305 310 315 320
Ile Ser Leu Cys Gln Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu
325 330 335

Lys Ile Leu Val Ala Leu Cys Gly Gly Asn

340

345

5 <210> 52

<211> 469

<212> PRT

<213> Homo sapiens

<220>

10 <221> Keratin, type II cytoskeletal 7

<222> (1)..(469)

<223> Accession No. as of 10 Dec 2002: P08729

<400> 52

15 Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala

1

5

10

15

Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly

20

25

30

Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg

20

35

40

45

Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg

50

55

60

Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Asp Ala

65

70

75

80

157/335

Asp Pro Ser Leu Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys
85 90 95

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
100 105 110

5 Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu
115 120 125

Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln
130 135 140

Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Leu Gln Val Asp Gly Gly
10 145 150 155 160

Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp Phe
165 170 175

Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu Asn
180 185 190

15 Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys
195 200 205

Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn Phe
210 215 220

Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln Ile
20 225 230 235 240

Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp
245 250 255

Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala
260 265 270

158/335

Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu
275 280 285

Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn Thr
290 295 300

5 Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala
305 310 315 320

Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile
325 330 335

Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala
10 340 345 350

Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met
355 360 365

Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala
370 375 380

15 Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu
385 390 395 400

Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Val Asn Ile Ser Val Met
405 410 415

Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr Leu
20 420 425 430

Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ser Ala Gly
435 440 445

Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser Arg
450 455 460

Arg Ser Ala Arg Asp

465

5 <210> 53

<211> 836

<212> PRT

<213> Homo sapiens

<220>

10 <221> Osteoblast specific factor 2 precursor

<222> (1)..(836)

<223> Accession No. as of 10 Dec 2002: Q15063

<400> 53

15 Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Ile Val

1 5 10 15

Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser

20 25 30

Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln

20 35 40 45

Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr

50 55 60

Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys

65 70 75 80

160/335

Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
85 90 95

Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
100 105 110

5 Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
115 120 125

Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn
130 135 140

Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu
10 145 150 155 160

Leu Leu Asn Ala Leu His Ser His Met Ile Asn Lys Arg Met Leu Thr
165 170 175

Lys Asp Leu Lys Asn Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu
180 185 190

15 Gly Leu Phe Ile Asn His Tyr Pro Asn Gly Val Val Thr Val Asn Cys
195 200 205

Ala Arg Ile Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val Val His
210 215 220

Val Ile Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe
20 225 230 235 240

Ile Glu Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr
245 250 255

Ser Asp Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe
260 265 270

161/335

Ala Pro Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu
275 280 285

Arg Phe Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His
290 295 300

5 Ile Leu Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val
305 310 315 320

Phe Glu Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp
325 330 335

Ser Ile Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val
10 340 345 350

Thr Asn Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp
355 360 365

Ser Ala Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe
370 375 380

15 Thr Asp Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp
385 390 395 400

Gly Glu Tyr Thr Leu Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp
405 410 415

Thr Leu Ser Met Val Gln Arg Leu Leu Lys Leu Ile Leu Gln Asn His
20 420 425 430

Ile Leu Lys Val Lys Val Gly Leu Asn Glu Leu Tyr Asn Gly Gln Ile
435 440 445

Leu Glu Thr Ile Gly Gly Lys Gln Leu Arg Val Phe Val Tyr Arg Thr
450 455 460

162/335

Ala Val Cys Ile Glu Asn Ser Cys Met Glu Lys Gly Ser Lys Gln Gly
465 470 475 480
Arg Asn Gly Ala Ile His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu
485 490 495
5 Lys Ser Leu His Glu Lys Leu Lys Gln Asp Lys Arg Phe Ser Thr Phe
500 505 510
Leu Ser Leu Leu Glu Ala Ala Asp Leu Lys Glu Leu Leu Thr Gln Pro
515 520 525
Gly Asp Trp Thr Leu Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met
10 530 535 540
Thr Ser Glu Glu Lys Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln
545 550 555 560
Asn Ile Ile Leu Tyr His Leu Thr Pro Gly Val Phe Ile Gly Lys Gly
565 570 575
15 Phe Glu Pro Gly Val Thr Asn Ile Leu Lys Thr Thr Gln Gly Ser Lys
580 585 590
Ile Phe Leu Lys Glu Val Asn Asp Thr Leu Leu Val Asn Glu Leu Lys
595 600 605
Ser Lys Glu Ser Asp Ile Met Thr Thr Asn Gly Val Ile His Val Val
20 610 615 620
Asp Lys Leu Leu Tyr Pro Ala Asp Thr Pro Val Gly Asn Asp Gln Leu
625 630 635 640
Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val
645 650 655

163/335

Arg Gly Ser Thr Phe Lys Glu Ile Pro Val Thr Val Tyr Thr Thr Lys
660 665 670
Ile Ile Thr Lys Val Val Glu Pro Lys Ile Lys Val Ile Glu Gly Ser
675 680 685
5 Leu Gln Pro Ile Ile Lys Thr Glu Gly Pro Thr Leu Thr Lys Val Lys
690 695 700
Ile Glu Gly Glu Pro Glu Phe Arg Leu Ile Lys Glu Gly Glu Thr Ile
705 710 715 720
Thr Glu Val Ile His Gly Glu Pro Ile Ile Lys Lys Tyr Thr Lys Ile
10 725 730 735
Ile Asp Gly Val Pro Val Glu Ile Thr Glu Lys Glu Thr Arg Glu Glu
740 745 750
Arg Ile Ile Thr Gly Pro Glu Ile Lys Tyr Thr Arg Ile Ser Thr Gly
755 760 765
15 Gly Gly Glu Thr Glu Glu Thr Leu Lys Lys Leu Leu Gln Glu Glu Val
770 775 780
Thr Lys Val Thr Lys Phe Ile Glu Gly Gly Asp Gly His Leu Phe Glu
785 790 795 800
Asp Glu Glu Ile Lys Arg Leu Leu Gln Gly Asp Thr Pro Val Arg Lys
20 805 810 815
Leu Gln Ala Asn Lys Lys Val Gln Gly Ser Arg Arg Arg Leu Arg Glu
820 825 830
Gly Arg Ser Gln
835

<210> 54
<211> 687
5 <212> PRT
<213> Homo sapiens
<220>
<221> Protein-glutamine gamma-glutamyltransferase
<222> (1)..(687)
10 <223> Accession No. P21980
<400> 54

Met Ala Glu Glu Leu Val Leu Glu Arg Cys Asp Leu Glu Leu Glu Thr
1 5 10 15
15 Asn Gly Arg Asp His His Thr Ala Asp Leu Cys Arg Glu Lys Leu Val
20 25 30
Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg
35 40 45
Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
20 50 55 60
Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
65 70 75 80
Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
85 90 95

165/335

Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
100 105 110

Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
115 120 125

5 Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
130 135 140

Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
145 150 155 160

Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
10 165 170 175

Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
180 185 190

Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly
195 200 205

15 Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Val
210 215 220

Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
225 230 235 240

Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly
20 245 250 255

Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
260 265 270

Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
275 280 285

166/335

Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
290 295 300
His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
305 310 315 320
5 Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys
325 330 335
Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
340 345 350
Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
10 355 360 365
Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly Asp Leu
370 375 380
Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
385 390 395 400
15 Val Val Asp Trp Ile Gln Gln Asp Asp Gly Ser Val His Lys Ser Ile
405 410 415
Asn Arg Ser Leu Ile Val Gly Leu Lys Ile Ser Thr Lys Ser Val Gly
420 425 430
Arg Asp Glu Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly
20 435 440 445
Ser Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys
450 455 460
Leu Ala Glu Lys Glu Glu Thr Gly Met Ala Met Arg Ile Arg Val Gly
465 470 475 480

Gln Ser Met Asn Met Gly Ser Asp Phe Asp Val Phe Ala His Ile Thr
485 490 495

Asn Asn Thr Ala Glu Glu Tyr Val Cys Arg Leu Leu Leu Cys Ala Arg
500 505 510

5 Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr
515 520 525

Leu Leu Asn Leu Asn Leu Glu Pro Phe Ser Glu Lys Ser Val Pro Leu
530 535 540

Cys Ile Leu Tyr Glu Lys Tyr Arg Asp Cys Leu Thr Glu Ser Asn Leu
10 545 550 555 560

Ile Lys Val Arg Ala Leu Leu Val Glu Pro Val Ile Asn Ser Tyr Leu
565 570 575

Leu Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg
580 585 590

15 Ile Leu Gly Glu Pro Lys Gln Lys Arg Lys Leu Val Ala Glu Val Ser
595 600 605

Leu Gln Asn Pro Leu Pro Val Ala Leu Glu Gly Cys Thr Phe Thr Val
610 615 620

Glu Gly Ala Gly Leu Thr Glu Glu Gln Lys Thr Val Glu Ile Pro Asp
20 625 630 635 640

Pro Val Glu Ala Gly Glu Glu Val Lys Val Arg Met Asp Leu Leu Pro
645 650 655

Leu His Met Gly Leu His Lys Leu Val Val Asn Phe Glu Ser Asp Lys
660 665 670

168/335

Leu Lys Ala Val Lys Gly Phe Arg Asn Val Ile Ile Gly Pro Ala

675

680

685

5 <210> 55

<211> 204

<212> PRT

<213> Homo sapiens

<220>

10 <221> Rho GDP-dissociation inhibitor 1

<222> (1)..(204)

<223> Accession No. as of 10 Dec 2002: P52565

<400> 55

15 Met Ala Glu Gln Glu Pro Thr Ala Glu Gln Leu Ala Gln Ile Ala Ala

1

5

10

15

Glu Asn Glu Glu Asp Glu His Ser Val Asn Tyr Lys Pro Pro Ala Gln

20

25

30

Lys Ser Ile Gln Glu Ile Gln Glu Leu Asp Lys Asp Asp Glu Ser Leu

20

35

40

45

Arg Lys Tyr Lys Glu Ala Leu Leu Gly Arg Val Ala Val Ser Ala Asp

50

55

60

Pro Asn Val Pro Asn Val Val Val Thr Gly Leu Thr Leu Val Cys Ser

65

70

75

80

169/335

Ser Ala Pro Gly Pro Leu Glu Leu Asp Leu Thr Gly Asp Leu Glu Ser
85 90 95
Phe Lys Lys Gln Ser Phe Val Leu Lys Glu Gly Val Glu Tyr Arg Ile
100 105 110
5 Lys Ile Ser Phe Arg Val Asn Arg Glu Ile Val Ser Gly Met Lys Tyr
115 120 125
Ile Gln His Thr Tyr Arg Lys Gly Val Lys Ile Asp Lys Thr Asp Tyr
130 135 140
Met Val Gly Ser Tyr Gly Pro Arg Ala Glu Glu Tyr Glu Phe Leu Thr
10 145 150 155 160
Pro Val Glu Glu Ala Pro Lys Gly Met Leu Ala Arg Gly Ser Tyr Ser
165 170 175
Ile Lys Ser Arg Phe Thr Asp Asp Asp Lys Thr Asp His Leu Ser Trp
180 185 190
15 Glu Trp Asn Leu Thr Ile Lys Lys Asp Trp Lys Asp
195 200

<210> 56

20 <211> 492

<212> PRT

<213> Homo sapiens

<220>

<221> Fascin 2

<222> (1) .. (492)

<223> Accession No. as of 29 August 2003: O14926

<400> 56

5 Met Pro Thr Asn Gly Leu His Gln Val Leu Lys Ile Gln Phe Gly Leu
1 5 10 15
Val Asn Asp Thr Asp Arg Tyr Leu Thr Ala Glu Ser Phe Gly Phe Lys
20 25 30
Val Asn Ala Ser Ala Pro Ser Leu Lys Arg Lys Gln Thr Trp Val Leu
10 35 40 45
Glu Pro Asp Pro Gly Gln Gly Thr Ala Val Leu Leu Arg Ser Ser His
50 55 60
Leu Gly Arg Tyr Leu Ser Ala Glu Glu Asp Gly Arg Val Ala Cys Glu
65 70 75 80
15 Ala Glu Gln Pro Gly Arg Asp Cys Arg Phe Leu Val Leu Pro Gln Pro
85 90 95
Asp Gly Arg Trp Val Leu Arg Ser Glu Pro His Gly Arg Phe Phe Gly
100 105 110
Gly Thr Glu Asp Gln Leu Ser Cys Phe Ala Thr Ala Val Ser Pro Ala
20 115 120 125
Glu Leu Trp Thr Val His Leu Ala Ile His Pro Gln Ala His Leu Leu
130 135 140
Ser Val Ser Arg Arg Arg Tyr Val His Leu Cys Pro Arg Glu Asp Glu
145 150 155 160

171/335

Met Ala Ala Asp Gly Asp Lys Pro Trp Gly Val Asp Ala Leu Leu Thr
165 170 175

Leu Ile Phe Arg Ser Arg Arg Tyr Cys Leu Lys Ser Cys Asp Ser Arg
180 185 190

5 Tyr Leu Arg Ser Asp Gly Arg Leu Val Trp Glu Pro Glu Pro Arg Ala
195 200 205

Cys Tyr Thr Leu Glu Phe Lys Ala Gly Lys Leu Ala Phe Lys Asp Cys
210 215 220

Asp Gly His Tyr Leu Ala Pro Val Gly Pro Ala Gly Thr Leu Lys Ala
10 225 230 235 240

Gly Arg Asn Thr Arg Pro Gly Lys Asp Glu Leu Phe Asp Leu Glu Glu
245 250 255

Ser His Pro Gln Val Val Leu Val Ala Ala Asn His Arg Tyr Val Ser
260 265 270

15 Val Arg Gln Gly Val Asn Val Ser Ala Asn Gln Asp Asp Glu Leu Asp
275 280 285

His Glu Thr Phe Leu Met Gln Ile Asp Gln Glu Thr Lys Lys Cys Thr
290 295 300

Phe Tyr Ser Ser Thr Gly Gly Tyr Trp Thr Leu Val Thr His Gly Gly
20 305 310 315 320

Ile His Ala Thr Ala Thr Gln Val Ser Ala Asn Thr Met Phe Glu Met
325 330 335

Glu Trp Arg Gly Arg Arg Val Ala Leu Lys Ala Ser Asn Gly Arg Tyr
340 345 350

172/335

Val Cys Met Lys Lys Asn Gly Gln Leu Ala Ala Ile Ser Asp Phe Val
355 360 365

Gly Lys Asp Glu Glu Phe Thr Leu Lys Leu Ile Asn Arg Pro Ile Leu
370 375 380

5 Val Leu Arg Gly Leu Asp Gly Phe Val Cys His His Arg Gly Ser Asn
385 390 395 400

Gln Leu Asp Thr Asn Arg Ser Val Tyr Asp Val Phe His Leu Ser Phe
405 410 415

Ser Asp Gly Ala Tyr Arg Ile Arg Gly Arg Asp Gly Gly Phe Trp Tyr
10 420 425 430

Thr Gly Ser His Gly Ser Val Cys Ser Asp Gly Glu Arg Ala Glu Asp
435 440 445

Phe Val Phe Glu Phe Arg Glu Arg Gly Arg Leu Ala Ile Arg Ala Arg
450 455 460

15 Ser Gly Lys Tyr Leu Arg Gly Gly Ala Ser Gly Leu Leu Arg Ala Asp
465 470 475 480

Ala Asp Ala Pro Ala Gly Thr Ala Leu Trp Glu Tyr
485 490

20

<210> 57

<211> 165

<212> PRT

<213> Homo sapiens

173/335

<220>

<221> Destrin (Actin-depolymerizing factor) (ADF)

<222> (1)..(165)

<223> Accession No. as of 29 August 2003: P18282

5 <400> 57

Met Ala Ser Gly Val Gln Val Ala Asp Glu Val Cys Arg Ile Phe Tyr
1 5 10 15
Asp Met Lys Val Arg Lys Cys Ser Thr Pro Glu Glu Ile Lys Lys Arg
10 20 25 30
Lys Lys Ala Val Ile Phe Cys Leu Ser Ala Asp Lys Lys Cys Ile Ile
35 40 45
Val Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Val Thr Ile
50 55 60
15 Thr Asp Pro Phe Lys His Phe Val Gly Met Leu Pro Glu Lys Asp Cys
65 70 75 80
Arg Tyr Ala Leu Tyr Asp Ala Ser Phe Glu Thr Lys Glu Ser Arg Lys
85 90 95
Glu Glu Leu Met Phe Phe Leu Trp Ala Pro Glu Leu Ala Pro Leu Lys
20 100 105 110
Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Phe
115 120 125
Gln Gly Ile Lys His Glu Cys Gln Ala Asn Gly Pro Glu Asp Leu Asn
130 135 140

174/335

Arg Ala Cys Ile Ala Glu Lys Leu Gly Gly Ser Leu Ile Val Ala Phe

145

150

155

160

Glu Gly Cys Pro Val

165

5

<210> 58

<211> 492

<212> PRT

10 <213> Homo sapiens

<220>

<221> Fascin

<222> (1)..(492)

<223> Accession No. as of 29 August 2003: Q16658

15 <400> 58

Thr Ala Asn Gly Thr Ala Glu Ala Val Gln Ile Gln Phe Gly Leu Ile

1

5

10

15

Asn Cys Gly Asn Lys Tyr Leu Thr Ala Glu Ala Phe Gly Phe Lys Val

20

20

25

30

Asn Ala Ser Ala Ser Ser Leu Lys Lys Lys Gln Ile Trp Thr Leu Glu

35

40

45

Gln Pro Pro Asp Glu Ala Gly Ser Ala Ala Val Cys Leu Arg Ser His

50

55

60

175/335

Leu Gly Arg Tyr Leu Ala Ala Asp Lys Asp Gly Asn Val Thr Cys Glu
65 70 75 80

Arg Glu Val Pro Gly Pro Asp Cys Arg Phe Leu Ile Val Ala His Asp
85 90 95

5 Asp Gly Arg Trp Ser Leu Gln Ser Glu Ala His Arg Arg Tyr Phe Gly
100 105 110

Gly Thr Glu Asp Arg Leu Ser Cys Phe Ala Gln Thr Val Ser Pro Ala
115 120 125

Glu Lys Trp Ser Val His Ile Ala Met His Pro Gln Val Asn Ile Tyr
10 130 135 140

Ser Val Thr Arg Lys Arg Tyr Ala His Leu Ser Ala Arg Pro Ala Asp
145 150 155 160

Glu Ile Ala Val Asp Arg Asp Val Pro Trp Gly Val Asp Ser Leu Ile
165 170 175

15 Thr Leu Ala Phe Gln Asp Gln Arg Tyr Ser Val Gln Thr Ala Asp His
180 185 190

Arg Phe Leu Arg His Asp Gly Arg Leu Val Ala Arg Pro Glu Pro Ala
195 200 205

Thr Gly Tyr Thr Leu Glu Phe Arg Ser Gly Lys Val Ala Phe Arg Asp
20 210 215 220

Cys Glu Gly Arg Tyr Leu Ala Pro Ser Gly Pro Ser Gly Thr Leu Lys
225 230 235 240

Ala Gly Lys Ala Thr Lys Val Gly Lys Asp Glu Leu Phe Ala Leu Glu
245 250 255

176/335

Gln Ser Cys Ala Gln Val Val Leu Gln Ala Ala Asn Glu Arg Asn Val
260 265 270

Ser Thr Arg Gln Gly Met Asp Leu Ser Ala Asn Gln Asp Glu Glu Thr
275 280 285

5 Asp Gln Glu Thr Phe Gln Leu Glu Ile Asp Arg Asp Thr Lys Lys Cys
290 295 300

Ala Phe Arg Thr His Thr Gly Lys Tyr Trp Thr Leu Thr Ala Thr Gly
305 310 315 320

Gly Val Gln Ser Thr Ala Ser Ser Lys Asn Ala Ser Cys Tyr Phe Asp
10 325 330 335

Ile Glu Trp Arg Asp Arg Arg Ile Thr Leu Arg Ala Ser Asn Gly Lys
340 345 350

Phe Val Thr Ser Lys Lys Asn Gly Gln Leu Ala Ala Ser Val Glu Thr
355 360 365

15 Ala Gly Asp Ser Glu Leu Phe Leu Met Lys Leu Ile Asn Arg Pro Ile
370 375 380

Ile Val Phe Arg Gly Glu His Gly Phe Ile Gly Cys Arg Lys Val Thr
385 390 395 400

Gly Thr Leu Asp Ala Asn Arg Ser Ser Tyr Asp Val Phe Gln Leu Glu
20 405 410 415

Phe Asn Asp Gly Ala Tyr Asn Ile Lys Asp Ser Thr Gly Lys Tyr Trp
420 425 430

Thr Val Gly Ser Asp Ser Ala Val Thr Ser Ser Gly Asp Thr Pro Val
435 440 445

177/335

Asp Phe Phe Phe Glu Phe Cys Asp Tyr Asn Lys Val Ala Ile Lys Val
450 455 460
Gly Gly Arg Tyr Leu Lys Gly Asp His Ala Gly Val Leu Lys Ala Ser
465 470 475 480
5 Ala Glu Thr Val Asp Pro Ala Ser Leu Trp Glu Tyr
485 490

<210> 59
10 <211> 317
<212> PRT
<213> Homo sapiens
<220>
<221> Apo-E precursor
15 <222> (1)..(317)
<223> Accession No. as of 29 August 2003: P02649
<400> 59

Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys
20 1 5 10 15
Gln Ala Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu
20 25 30
Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu
35 40 45

178/335

Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln
50 55 60
Val Gln Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala
65 70 75 80
5 Leu Met Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu
85 90 95
Glu Glu Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser
100 105 110
Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp
10 115 120 125
Val Cys Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu
130 135 140
Gly Gln Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg
145 150 155 160
15 Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg
165 170 175
Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu
180 185 190
Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val
20 195 200 205
Arg Ala Ala Thr Val Gly Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg
210 215 220
Ala Gln Ala Trp Gly Glu Arg Leu Arg Ala Arg Met Glu Glu Met Gly
225 230 235 240

179/335

Ser Arg Thr Arg Asp Arg Leu Asp Glu Val Lys Glu Gln Val Ala Glu
245 250 255
Val Arg Ala Lys Leu Glu Glu Gln Ala Gln Gln Ile Arg Leu Gln Ala
260 265 270
5 Glu Ala Phe Gln Ala Arg Leu Lys Ser Trp Phe Glu Pro Leu Val Glu
275 280 285
Asp Met Gln Arg Gln Trp Ala Gly Leu Val Glu Lys Val Gln Ala Ala
290 295 300
Val Gly Thr Ser Ala Ala Pro Val Pro Ser Asp Asn His
10 305 310 315

<210> 60
<211> 838
15 <212> PRT
<213> Homo sapiens
<220>
<221> hypothetical 88.6 kDa protein
<222> (1)..(838)
20 <223> Accession No. as of 29 August 2003: Q96C61
<400> 60

Met Pro Ser Gly Lys Val Ala Gln Pro Thr Ile Thr Asp Asn Lys Asp

1

5

10

15

180/335

Gly Thr Val Thr Val Arg Tyr Ala Pro Ser Glu Ala Gly Leu His Glu
20 25 30
Met Asp Ile Arg Tyr Asp Asn Met His Ile Pro Gly Ser Pro Leu Gln
35 40 45
5 Phe Tyr Val Asp Tyr Val Asn Cys Gly His Val Thr Ala Tyr Gly Pro
50 55 60
Gly Leu Thr His Gly Val Val Asn Lys Pro Ala Thr Phe Thr Val Asn
65 70 75 80
Thr Lys Asp Ala Gly Glu Gly Gly Leu Ser Leu Ala Ile Glu Gly Pro
10 85 90 95
Ser Lys Ala Glu Ile Ser Cys Thr Asp Asn Gln Asp Gly Thr Cys Ser
100 105 110
Val Ser Tyr Leu Pro Val Leu Pro Gly Asp Tyr Ser Ile Leu Val Lys
115 120 125
15 Tyr Asn Glu Gln His Val Pro Gly Ser Pro Phe Thr Ala Arg Val Thr
130 135 140
Gly Asp Asp Ser Met Arg Met Ser His Leu Lys Val Gly Ser Ala Ala
145 150 155 160
Asp Ile Pro Ile Asn Ile Ser Glu Thr Asp Leu Ser Leu Leu Thr Ala
20 165 170 175
Thr Val Val Pro Pro Ser Gly Arg Glu Glu Pro Cys Leu Leu Lys Arg
180 185 190
Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro Lys Glu Thr Gly
195 200 205

181/335

Glu His Leu Val His Val Lys Lys Asn Gly Gln His Val Ala Ser Ser
210 215 220
Pro Ile Pro Val Val Ile Ser Gln Ser Glu Ile Gly Asp Ala Ser Arg
225 230 235 240
5 Val Arg Val Ser Gly Gln Gly Leu His Glu Gly His Thr Phe Glu Pro
245 250 255
Ala Glu Phe Ile Ile Asp Thr Arg Asp Ala Gly Tyr Gly Gly Leu Ser
260 265 270
Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn Thr Glu Asp Leu
10 275 280 285
Glu Asp Gly Thr Cys Arg Val Thr Tyr Cys Pro Thr Glu Pro Gly Asn
290 295 300
Tyr Ile Ile Asn Ile Lys Phe Ala Asp Gln His Val Pro Gly Ser Pro
305 310 315 320
15 Phe Ser Val Lys Val Thr Gly Glu Gly Arg Val Lys Glu Ser Ile Thr
325 330 335
Arg Arg Arg Arg Ala Pro Ser Val Ala Asn Val Gly Ser His Cys Asp
340 345 350
Leu Ser Leu Lys Ile Pro Glu Ile Ser Ile Gln Asp Met Thr Ala Gln
20 355 360 365
Val Thr Ser Pro Ser Gly Lys Thr His Glu Ala Glu Ile Val Glu Gly
370 375 380
Glu Asn His Thr Tyr Cys Ile Arg Phe Val Pro Ala Glu Met Gly Thr
385 390 395 400

182/335

His Thr Val Ser Val Lys Tyr Lys Gly Gln His Val Pro Gly Ser Pro
405 410 415

Phe Gln Phe Thr Val Gly Pro Leu Gly Glu Gly Gly Ala His Lys Val
420 425 430

5 Arg Ala Gly Gly Pro Gly Leu Glu Arg Ala Glu Ala Gly Val Pro Ala
435 440 445

Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly Ala Gly Gly Leu Ala Ile
450 455 460

Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Ser Phe Glu Asp Arg Lys
10 465 470 475 480

Asp Gly Ser Cys Gly Val Ala Tyr Val Val Gln Glu Pro Gly Asp Tyr
485 490 495

Glu Val Ser Val Lys Phe Asn Glu Glu His Ile Pro Asp Ser Pro Phe
500 505 510

15 Val Val Pro Val Ala Ser Pro Ser Gly Asp Ala Arg Arg Leu Thr Val
515 520 525

Ser Ser Leu Gln Glu Ser Gly Leu Lys Val Asn Gln Pro Ala Ser Phe
530 535 540

Ala Val Ser Leu Asn Gly Ala Lys Gly Ala Ile Asp Ala Lys Val His
20 545 550 555 560

Ser Pro Ser Gly Ala Leu Glu Glu Cys Tyr Val Thr Glu Ile Asp Gln
565 570 575

Asp Lys Tyr Ala Val Arg Phe Ile Pro Arg Glu Asn Gly Val Tyr Leu
580 585 590

Ile Asp Val Lys Phe Asn Gly Thr His Ile Pro Gly Ser Pro Phe Lys
595 600 605

Ile Arg Val Gly Glu Pro Gly His Gly Gly Asp Pro Gly Leu Val Ser
610 615 620

5 Ala Tyr Gly Ala Gly Leu Glu Gly Gly Val Thr Gly Asn Pro Ala Glu
625 630 635 640

Phe Val Val Asn Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser Val Thr
645 650 655

Ile Asp Gly Pro Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro Glu
10 660 665 670

Gly Tyr Arg Val Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu Ile
675 680 685

Ser Ile Lys Tyr Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe Lys
690 695 700

15 Ala Lys Val Thr Gly Pro Arg Leu Val Ser Asn His Ser Leu His Glu
705 710 715 720

Thr Ser Ser Val Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala Pro
725 730 735

Gln His Gly Ala Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val Val
20 740 745 750

Ala Lys Gly Leu Gly Leu Ser Lys Ala Tyr Val Gly Gln Lys Ser Ser
755 760 765

Phe Thr Val Asp Cys Ser Lys Ala Gly Asn Asn Met Leu Leu Val Gly
770 775 780

184/335

Val His Gly Pro Arg Thr Pro Cys Glu Glu Ile Leu Val Lys His Val

785

790

795

800

Gly Ser Arg Leu Tyr Ser Val Ser Tyr Leu Leu Lys Asp Lys Gly Glu

805

810

815

5 Tyr Thr Leu Val Val Lys Trp Gly Asp Glu His Ile Pro Gly Ser Pro

820

825

830

Tyr Arg Val Val Val Pro

835

10

<210> 61

<211> 433

<212> PRT

<213> Homo sapiens

15 <220>

<221> human alpha enolase

<222> (1)..(433)

<223> Accession No. as of 29 August 2003: P06733

<400> 61

20

Ser Ile Leu Lys Ile His Ala Arg Glu Ile Phe Asp Ser Arg Gly Asn

1

5

10

15

Pro Thr Val Glu Val Asp Leu Phe Thr Ser Lys Gly Leu Phe Arg Ala

20

25

30

185/335

Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala Leu Glu Leu
35 40 45

Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Lys Gly Val Ser Lys Ala
50 55 60

5 Val Glu His Ile Asn Lys Thr Ile Ala Pro Ala Leu Val Ser Lys Lys
65 70 75 80

Leu Asn Val Thr Glu Gln Glu Lys Ile Asp Lys Leu Met Ile Glu Met
85 90 95

Asp Gly Thr Glu Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu Gly
10 100 105 110

Val Ser Leu Ala Val Cys Lys Ala Gly Ala Val Glu Lys Gly Val Pro
115 120 125

Leu Tyr Arg His Ile Ala Asp Leu Ala Gly Asn Ser Glu Val Ile Leu
130 135 140

15 Pro Val Pro Ala Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly Asn
145 150 155 160

Lys Leu Ala Met Gln Glu Phe Met Ile Leu Pro Val Gly Ala Ala Asn
165 170 175

Phe Arg Glu Ala Met Arg Ile Gly Ala Glu Val Tyr His Asn Leu Lys
180 185 190

20 Asn Val Ile Lys Glu Lys Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp
195 200 205

Glu Gly Gly Phe Ala Pro Asn Ile Leu Glu Asn Lys Glu Gly Leu Glu
210 215 220

186/335

Leu Leu Lys Thr Ala Ile Gly Lys Ala Gly Tyr Thr Asp Lys Val Val
225 230 235 240
Ile Gly Met Asp Val Ala Ala Ser Glu Phe Phe Arg Ser Gly Lys Tyr
245 250 255
5 Asp Leu Asp Phe Lys Ser Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro
260 265 270
Asp Gln Leu Ala Asp Leu Tyr Lys Ser Phe Ile Lys Asp Tyr Pro Val
275 280 285
Val Ser Ile Glu Asp Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp Gln
10 290 295 300
Lys Phe Thr Ala Ser Ala Gly Ile Gln Val Val Gly Asp Asp Leu Thr
305 310 315 320
Val Thr Asn Pro Lys Arg Ile Ala Lys Ala Val Asn Glu Lys Ser Cys
325 330 335
15 Asn Cys Leu Leu Leu Lys Val Asn Gln Ile Gly Ser Val Thr Glu Ser
340 345 350
Leu Gln Ala Cys Lys Leu Ala Gln Ala Asn Gly Trp Gly Val Met Val
355 360 365
Ser His Arg Ser Gly Glu Thr Glu Asp Thr Phe Ile Ala Asp Leu Val
20 370 375 380
Val Gly Leu Cys Thr Gly Gln Ile Lys Thr Gly Ala Pro Cys Arg Ser
385 390 395 400
Glu Arg Leu Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu Glu Glu Leu
405 410 415

187/335

Gly Ser Lys Ala Lys Phe Ala Gly Arg Asn Phe Arg Asn Pro Leu Ala

420

425

430

Lys

5

<210> 62

<211> 471

<212> PRT

10 <213> Homo sapiens

<220>

<221> tryptophanyl-tRNA synthetase

<222> (1)..(471)

<223> Accession No. as of 29 August 2003: P23381

15 <400> 62

Met Pro Asn Ser Glu Pro Ala Ser Leu Leu Glu Leu Phe Asn Ser Ile

1

5

10

15

Ala Thr Gln Gly Glu Leu Val Arg Ser Leu Lys Ala Gly Asn Ala Ser

20

20

25

30

Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu Lys Met

35

40

45

Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro

50

55

60

188/335

Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala
 65 70 75 80
 Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys
 85 90 95
 5 Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile
 100 105 110
 Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro
 115 120 125
 His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn
 10 130 135 140
 Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr
 145 150 155 160
 Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro
 165 170 175
 15 Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val
 180 185 190
 Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu
 195 200 205
 Asp Gln Ala Tyr Ser Tyr Ala Val Glu Asn Ala Lys Asp Ile Ile Ala
 20 210 215 220
 Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr
 225 230 235 240
 Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys
 245 250 255

189/335

His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser
260 265 270
Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser
275 280 285
5 Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln
290 295 300
Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr
305 310 315 320
Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His
10 325 330 335
Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala
340 345 350
Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile
355 360 365
15 Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile
370 375 380
Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe
385 390 395 400
Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile
20 405 410 415
Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys
420 425 430
Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg
435 440 445

190/335

Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg

450

455

460

Lys Leu Ser Phe Asp Phe Gln

465

470

5

<210> 63

<211> 106

<212> PRT

10 <213> Homo sapiens

<220>

<221> Ig kappa chain C regionI

<222> (1)..(106)

<223> Accession No. as of 29 August 2003: P01834

15 <400> 63

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln

1

5

10

15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr

20

20

25

30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser

35

40

45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr

50

55

60

191/335

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys

65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro

85 90 95

5 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

100 105

<210> 64

10 <211> 758

<212> PRT

<213> Homo sapiens

<220>

<221> Mitofilin

15 <222> (1)..(758)

<223> Accession No. as of 29 August 2003: Q16891

<400> 64

Met Leu Arg Ala Cys Gln Leu Ser Gly Val Thr Ala Ala Ala Gln Ser

20 1 5 10 15

Cys Leu Cys Gly Lys Phe Val Leu Arg Pro Leu Arg Pro Cys Arg Arg

20 25 30

Tyr Ser Thr Ser Gly Ser Ser Gly Leu Thr Thr Gly Lys Ile Ala Gly

35 40 45

192/335

Ala Gly Leu Leu Phe Val Gly Gly Gly Ile Gly Gly Thr Ile Leu Tyr
50 55 60

Ala Lys Trp Asp Ser His Phe Arg Glu Ser Val Glu Lys Thr Ile Pro
65 70 75 80

5 Tyr Ser Asp Lys Leu Phe Glu Met Val Leu Gly Pro Ala Ala Tyr Asn
85 90 95

Val Pro Leu Pro Lys Lys Ser Ile Gln Ser Gly Pro Leu Lys Ile Ser
100 105 110

Ser Val Ser Glu Val Met Lys Glu Ser Lys Gln Pro Ala Ser Gln Leu
10 115 120 125

Gln Lys Gln Lys Gly Asp Thr Pro Ala Ser Ala Thr Ala Pro Thr Glu
130 135 140

Ala Ala Gln Ile Ile Ser Ala Ala Gly Asp Thr Leu Ser Val Pro Ala
145 150 155 160

15 Pro Ala Val Gln Pro Glu Glu Ser Leu Lys Thr Asp His Pro Glu Ile
165 170 175

Gly Glu Gly Lys Pro Thr Pro Ala Leu Ser Glu Glu Ala Ser Ser Ser
180 185 190

Ser Ile Arg Glu Arg Pro Pro Glu Glu Val Ala Ala Arg Leu Ala Gln
20 195 200 205

Gln Glu Lys Gln Glu Gln Val Lys Ile Glu Ser Leu Ala Lys Ser Leu
210 215 220

Glu Asp Ala Leu Arg Gln Thr Ala Ser Val Thr Leu Gln Ala Ile Ala
225 230 235 240

Ala Gln Asn Ala Ala Val Gln Ala Val Asn Ala His Ser Asn Ile Leu
245 250 255

Lys Ala Ala Met Asp Asn Ser Glu Ile Ala Gly Glu Lys Lys Ser Ala
260 265 270

5 Gln Trp Arg Thr Val Glu Gly Ala Leu Lys Glu Arg Arg Lys Ala Val
275 280 285

Asp Glu Ala Ala Asp Ala Leu Leu Lys Ala Lys Glu Glu Leu Glu Lys
290 295 300

Met Lys Ser Val Ile Glu Asn Ala Lys Lys Lys Glu Val Ala Gly Ala
10 305 310 315 320

Lys Pro His Ile Thr Ala Ala Glu Gly Lys Leu His Asn Met Ile Val
325 330 335

Asp Leu Asp Asn Val Val Lys Lys Val Gln Ala Ala Gln Ser Glu Ala
340 345 350

15 Lys Val Val Ser Gln Tyr His Glu Leu Val Val Gln Ala Arg Asp Asp
355 360 365

Phe Lys Arg Glu Leu Asp Ser Ile Thr Pro Glu Val Leu Pro Gly Trp
370 375 380

Lys Gly Met Ser Val Ser Asp Leu Ala Asp Lys Leu Ser Thr Asp Asp
20 385 390 395 400

Leu Asn Ser Leu Ile Ala His Ala His Arg Arg Ile Asp Gln Leu Asn
405 410 415

Arg Glu Leu Ala Glu Gln Lys Ala Thr Glu Lys Gln His Ile Thr Leu
420 425 430

194/335

Ala Leu Glu Lys Gln Lys Leu Glu Glu Lys Arg Ala Phe Asp Ser Ala
435 440 445

Val Ala Lys Ala Leu Glu His His Arg Ser Glu Ile Gln Ala Glu Gln
450 455 460

5 Asp Arg Lys Ile Glu Glu Val Arg Asp Ala Met Glu Asn Glu Met Arg
465 470 475 480

Thr Gln Leu Arg Arg Gln Ala Ala Ala His Thr Asp His Leu Arg Asp
485 490 495

Val Leu Arg Val Gln Glu Gln Glu Leu Lys Ser Glu Phe Glu Gln Asn
10 500 505 510

Leu Ser Glu Lys Leu Ser Glu Gln Glu Leu Gln Phe Arg Arg Leu Ser
515 520 525

Gln Glu Gln Val Asp Asn Phe Thr Leu Asp Ile Asn Thr Ala Tyr Ala
530 535 540

15 Arg Leu Arg Gly Ile Glu Gln Ala Val Gln Ser His Ala Val Ala Glu
545 550 555 560

Glu Glu Ala Arg Lys Ala His Gln Leu Trp Leu Ser Val Glu Ala Leu
565 570 575

Lys Tyr Ser Met Lys Thr Ser Ser Ala Glu Thr Pro Thr Ile Pro Leu
20 580 585 590

Gly Ser Ala Val Glu Ala Ile Lys Ala Asn Cys Ser Asp Asn Glu Phe
595 600 605

Thr Gln Ala Leu Thr Ala Ala Ile Pro Pro Glu Ser Leu Thr Arg Gly
610 615 620

195/335

Val Tyr Ser Glu Glu Thr Leu Arg Ala Arg Phe Tyr Ala Val Gln Lys
625 630 635 640
Leu Ala Arg Arg Val Ala Met Ile Asp Glu Thr Arg Asn Ser Leu Tyr
645 650 655
5 Gln Tyr Phe Leu Ser Tyr Leu Gln Ser Leu Leu Leu Phe Pro Pro Gln
660 665 670
Gln Leu Lys Pro Pro Pro Glu Leu Cys Pro Glu Asp Ile Asn Thr Phe
675 680 685
Lys Leu Leu Ser Tyr Ala Ser Tyr Cys Ile Glu His Gly Asp Leu Glu
10 690 695 700
Leu Ala Ala Lys Phe Val Asn Gln Leu Lys Gly Glu Ser Arg Arg Val
705 710 715 720
Ala Gln Asp Trp Leu Lys Glu Ala Arg Met Thr Leu Glu Thr Lys Gln
725 730 735
15 Ile Val Glu Ile Leu Thr Ala Tyr Ala Ser Ala Val Gly Ile Gly Thr
740 745 750
Thr Gln Val Gln Pro Glu
755

20

<210> 65

<211> 1410

<212> PRT

<213> Homo sapiens

<220>

<221> Ribosome-binding protein 1

<222> (1)..(1410)

<223> Accession No. as of 29 August 2003: 075300

5 <400> 65

Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly Gly
1 5 10 15
Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
10 20 25 30
Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
35 40 45
Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
50 55 60
15 Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65 70 75 80
Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
85 90 95
Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
20 100 105 110
Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met Pro
115 120 125
Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
130 135 140

197/335

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
145 150 155 160
Gln Val Leu Thr Ser Lys Ala Ala Ile Leu Glu Thr Ala Pro Lys Glu
165 170 175
5 Val Pro Met Val Val Val Pro Pro Val Gly Ala Lys Gly Asn Thr Pro
180 185 190
Ala Thr Gly Thr Thr Gln Gly Lys Lys Ala Glu Gly Thr Gln Asn Gln
195 200 205
Ser Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu Gly
10 210 215 220
Thr Pro Asn Gln Gly Lys Lys Thr Glu Gly Thr Pro Asn Gln Gly Lys
225 230 235 240
Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
245 250 255
15 Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val
260 265 270
Asp Thr Thr Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Pro Thr Gln
275 280 285
Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Ala Lys Lys Val Glu Gly
20 290 295 300
Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
305 310 315 320
Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
325 330 335

198/335

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
340 345 350

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
355 360 365

5 Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ser Glu Gly
370 375 380

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys
385 390 395 400

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
10 405 410 415

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
420 425 430

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
435 440 445

15 Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
450 455 460

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys
465 470 475 480

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
20 485 490 495

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Gln Lys Gly
500 505 510

Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Gln Gly Lys
515 520 525

Lys Ala Glu Arg Ser Pro Asn Gln Gly Lys Lys Gly Glu Gly Ala Pro
530 535 540
Ile Gln Gly Lys Lys Ala Asp Ser Val Ala Asn Gln Gly Thr Lys Val
545 550 555 560
5 Glu Gly Ile Thr Asn Gln Gly Lys Lys Ala Glu Gly Ser Pro Ser Glu
565 570 575
Gly Lys Lys Ala Glu Gly Ser Pro Asn Gln Gly Lys Lys Ala Asp Ala
580 585 590
Ala Ala Asn Gln Gly Lys Lys Thr Glu Ser Ala Ser Val Gln Gly Arg
10 595 600 605
Asn Thr Asp Val Ala Gln Ser Pro Glu Ala Pro Lys Gln Glu Ala Pro
610 615 620
Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Glu Pro Gly Pro Pro
625 630 635 640
15 Asp Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val Ser Thr
645 650 655
Val Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu Ile Glu
660 665 670
Ile Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His Lys Ala
20 675 680 685
Thr Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu
690 695 700
Lys Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys
705 710 715 720

200/335

Ser Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys Ala Lys
725 730 735

Ala Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu
740 745 750

5 Gln Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu
755 760 765

His Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln
770 775 780

Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln
10 785 790 795 800

Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val
805 810 815

Glu Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser
820 825 830

15 Lys Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Val Arg Gln Asp
835 840 845

Glu Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe Glu Lys
850 855 860

Gln Val Leu Gln Leu Gln Ala Ser His Arg Glu Ser Glu Glu Ala Leu
20 865 870 875 880

Gln Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys His Thr Gln Ser
885 890 895

Ser His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln
900 905 910

201/335

Gln Gln Met Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Ala Glu
 915 920 925
 Val Arg Ser Lys Cys Glu Glu Leu Ser Gly Leu His Gly Gln Leu Gln
 930 935 940
 5 Glu Ala Arg Ala Glu Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile
 945 950 955 960
 Glu Ala Leu Leu Glu Ala Gly Gln Ala Arg Asp Ala Gln Asp Val Gln
 965 970 975
 Ala Ser Gln Ala Glu Ala Asp Gln Gln Gln Thr Arg Leu Lys Glu Leu
 10 980 985 990
 Glu Ser Gln Val Ser Gly Leu Glu Lys Glu Ala Ile Glu Leu Arg Glu
 995 1000 1005
 Ala Val Glu Gln Gln Lys Val Lys Asn Asn Asp Leu Arg Glu Lys
 1010 1015 1020
 15 Asn Trp Lys Ala Met Glu Ala Leu Ala Thr Ala Glu Gln Ala Cys
 1025 1030 1035
 Lys Glu Lys Leu Leu Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu
 1040 1045 1050
 Lys Gln Leu Cys Leu Ile Glu Ala Gln Thr Met Glu Ala Leu Leu
 20 1055 1060 1065
 Ala Leu Leu Pro Glu Leu Ser Val Leu Ala Gln Gln Asn Tyr Thr
 1070 1075 1080
 Glu Trp Leu Gln Asp Leu Lys Glu Lys Gly Pro Thr Leu Leu Lys
 1085 1090 1095

	His Pro	Pro Ala	Pro Ala	Glu	Pro Ser	Ser Asp	Leu	Ala Ser	Lys
	1100			1105			1110		
	Leu Arg	Glu Ala	Glu Glu	Thr	Gln Ser	Thr Leu	Gln	Ala Glu	Cys
	1115			1120			1125		
5	Asp Gln	Tyr Arg	Ser Ile	Leu	Ala Glu	Thr Glu	Gly	Met Leu	Arg
	1130			1135			1140		
	Asp Leu	Gln Lys	Ser Val	Glu	Glu Glu	Glu Gln	Val	Trp Arg	Ala
	1145			1150			1155		
	Lys Val	Gly Ala	Ala Glu	Glu	Glu Leu	Gln Lys	Ser	Arg Val	Thr
10	1160			1165			1170		
	Val Lys	His Leu	Glu Glu	Ile	Val Glu	Lys Leu	Lys	Gly Glu	Leu
	1175			1180			1185		
	Glu Ser	Ser Asp	Gln Val	Arg	Glu His	Thr Ser	His	Leu Glu	Ala
	1190			1195			1200		
15	Glu Leu	Glu Lys	His Met	Ala	Ala Ala	Ser Ala	Glu	Cys Gln	Asn
	1205			1210			1215		
	Tyr Ala	Lys Glu	Val Ala	Gly	Leu Arg	Gln Leu	Leu	Leu Glu	Ser
	1220			1225			1230		
	Gln Ser	Gln Leu	Asp Ala	Ala	Lys Ser	Glu Ala	Gln	Lys Gln	Ser
20	1235			1240			1245		
	Asp Glu	Leu Ala	Leu Val	Arg	Gln Gln	Leu Ser	Glu	Met Lys	Ser
	1250			1255			1260		
	His Val	Glu Asp	Gly Asp	Ile	Ala Gly	Ala Pro	Ala	Ser Ser	Pro
	1265			1270			1275		

203/335

Glu Ala Pro Pro Ala Glu Gln Asp Pro Val Gln Leu Lys Thr Gln
1280 1285 1290
Leu Glu Trp Thr Glu Ala Ile Leu Glu Asp Glu Gln Thr Gln Arg
1295 1300 1305
5 Gln Lys Leu Thr Ala Glu Phe Glu Glu Ala Gln Thr Ser Ala Cys
1310 1315 1320
Arg Leu Gln Glu Glu Leu Glu Lys Leu Arg Thr Ala Gly Pro Leu
1325 1330 1335
Glu Ser Ser Glu Thr Glu Glu Ala Ser Gln Leu Lys Glu Arg Leu
10 1340 1345 1350
Glu Lys Glu Lys Lys Leu Thr Ser Asp Leu Gly Arg Ala Ala Thr
1355 1360 1365
Arg Leu Gln Glu Leu Leu Lys Thr Thr Gln Glu Gln Leu Ala Arg
1370 1375 1380
15 Glu Lys Asp Thr Val Lys Lys Leu Gln Glu Gln Leu Glu Lys Ala
1385 1390 1395
Glu Asp Gly Ser Ser Ser Lys Glu Gly Thr Ser Val
1400 1405 1410

20

<210> 66

<211> 453

<212> PRT

<213> Homo sapiens

<220>

<221> Fibrinogen gamma chain precursor

<222> (1)..(453)

<223> Accession No. as of 29 August 2003: P02679

5 <400> 66

Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala

1 5 10 15

Leu Leu Phe Leu Ser Ser Thr Cys Val Ala Tyr Val Ala Thr Arg Asp

10 20 25 30

Asn Cys Cys Ile Leu Asp Glu Arg Phe Gly Ser Tyr Cys Pro Thr Thr

35 40 45

Cys Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys

50 55 60

15 Asp Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr

65 70 75 80

Ser Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro

85 90 95

Asp Glu Ser Ser Lys Pro Asn Met Ile Asp Ala Ala Thr Leu Lys Ser

20 100 105 110

Arg Lys Met Leu Glu Glu Ile Met Lys Tyr Glu Ala Ser Ile Leu Thr

115 120 125

His Asp Ser Ser Ile Arg Tyr Leu Gln Glu Ile Tyr Asn Ser Asn Asn

130 135 140

205/335

Gln Lys Ile Val Asn Leu Lys Glu Lys Val Ala Gln Leu Glu Ala Gln
145 150 155 160
Cys Gln Glu Pro Cys Lys Asp Thr Val Gln Ile His Asp Ile Thr Gly
165 170 175
5 Lys Asp Cys Gln Asp Ile Ala Asn Lys Gly Ala Lys Gln Ser Gly Leu
180 185 190
Tyr Phe Ile Lys Pro Leu Lys Ala Asn Gln Gln Phe Leu Val Tyr Cys
195 200 205
Glu Ile Asp Gly Ser Gly Asn Gly Trp Thr Val Phe Gln Lys Arg Leu
10 210 215 220
Asp Gly Ser Val Asp Phe Lys Lys Asn Trp Ile Gln Tyr Lys Glu Gly
225 230 235 240
Phe Gly His Leu Ser Pro Thr Gly Thr Thr Glu Phe Trp Leu Gly Asn
245 250 255
15 Glu Lys Ile His Leu Ile Ser Thr Gln Ser Ala Ile Pro Tyr Ala Leu
260 265 270
Arg Val Glu Leu Glu Asp Trp Asn Gly Arg Thr Ser Thr Ala Asp Tyr
275 280 285
Ala Met Phe Lys Val Gly Pro Glu Ala Asp Lys Tyr Arg Leu Thr Tyr
20 290 295 300
Ala Tyr Phe Ala Gly Gly Asp Ala Gly Asp Ala Phe Asp Gly Phe Asp
305 310 315 320
Phe Gly Asp Asp Pro Ser Asp Lys Phe Phe Thr Ser His Asn Gly Met
325 330 335

206/335

Gln Phe Ser Thr Trp Asp Asn Asp Asn Asp Lys Phe Glu Gly Asn Cys
340 345 350

Ala Glu Gln Asp Gly Ser Gly Trp Trp Met Asn Lys Cys His Ala Gly
355 360 365

5 His Leu Asn Gly Val Tyr Tyr Gln Gly Gly Thr Tyr Ser Lys Ala Ser
370 375 380

Thr Pro Asn Gly Tyr Asp Asn Gly Ile Ile Trp Ala Thr Trp Lys Thr
385 390 395 400

Arg Trp Tyr Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn
10 405 410 415

Arg Leu Thr Ile Gly Glu Gly Gln Gln His His Leu Gly Gly Ala Lys
420 425 430

Gln Val Arg Pro Glu His Pro Ala Glu Thr Glu Tyr Asp Ser Leu Tyr
435 440 445

15 Pro Glu Asp Asp Leu
450

<210> 67

20 <211> 622

<212> PRT

<213> Homo sapiens

<220>

<221> Prothrombin precursor

<222> (1)..(622)

<223> Accession No. as of 29 August 2003: P00734

<400> 67

5 Met Ala His Val Arg Gly Leu Gln Leu Pro Gly Cys Leu Ala Leu Ala

1 5 10 15

Ala Leu Cys Ser Leu Val His Ser Gln His Val Phe Leu Ala Pro Gln

20 25 30

Gln Ala Arg Ser Leu Leu Gln Arg Val Arg Arg Ala Asn Thr Phe Leu

10 35 40 45

Glu Glu Val Arg Lys Gly Asn Leu Glu Arg Glu Cys Val Glu Glu Thr

50 55 60

Cys Ser Tyr Glu Glu Ala Phe Glu Ala Leu Glu Ser Ser Thr Ala Thr

65 70 75 80

15 Asp Val Phe Trp Ala Lys Tyr Thr Ala Cys Glu Thr Ala Arg Thr Pro

85 90 95

Arg Asp Lys Leu Ala Ala Cys Leu Glu Gly Asn Cys Ala Glu Gly Leu

100 105 110

Gly Thr Asn Tyr Arg Gly His Val Asn Ile Thr Arg Ser Gly Ile Glu

20 115 120 125

Cys Gln Leu Trp Arg Ser Arg Tyr Pro His Lys Pro Glu Ile Asn Ser

130 135 140

Thr Thr His Pro Gly Ala Asp Leu Gln Glu Asn Phe Cys Arg Asn Pro

145 150 155 160

208/335

Asp Ser Ser Thr Thr Gly Pro Trp Cys Tyr Thr Thr Asp Pro Thr Val
165 170 175

Arg Arg Gln Glu Cys Ser Ile Pro Val Cys Gly Gln Asp Gln Val Thr
180 185 190

5 Val Ala Met Thr Pro Arg Ser Glu Gly Ser Ser Val Asn Leu Ser Pro
195 200 205

Pro Leu Glu Gln Cys Val Pro Asp Arg Gly Gln Gln Tyr Gln Gly Arg
210 215 220

Leu Ala Val Thr Thr His Gly Leu Pro Cys Leu Ala Trp Ala Ser Ala
10 225 230 235 240

Gln Ala Lys Ala Leu Ser Lys His Gln Asp Phe Asn Ser Ala Val Gln
245 250 255

Leu Val Glu Asn Phe Cys Arg Asn Pro Asp Gly Asp Glu Glu Gly Val
260 265 270

15 Trp Cys Tyr Val Ala Gly Lys Pro Gly Asp Phe Gly Tyr Cys Asp Leu
275 280 285

Asn Tyr Cys Glu Glu Ala Val Glu Glu Glu Thr Gly Asp Gly Leu Asp
290 295 300

Glu Asp Ser Asp Arg Ala Ile Glu Gly Arg Thr Ala Thr Ser Glu Tyr
20 305 310 315 320

Gln Thr Phe Phe Asn Pro Arg Thr Phe Gly Ser Gly Glu Ala Asp Cys
325 330 335

Gly Leu Arg Pro Leu Phe Glu Lys Lys Ser Leu Glu Asp Lys Thr Glu
340 345 350

Arg Glu Leu Leu Glu Ser Tyr Ile Asp Gly Arg Ile Val Glu Gly Ser
355 360 365

Asp Ala Glu Ile Gly Met Ser Pro Trp Gln Val Met Leu Phe Arg Lys
370 375 380

5 Ser Pro Gln Glu Leu Leu Cys Gly Ala Ser Leu Ile Ser Asp Arg Trp
385 390 395 400

Val Leu Thr Ala Ala His Cys Leu Leu Tyr Pro Pro Trp Asp Lys Asn
405 410 415

Phe Thr Glu Asn Asp Leu Leu Val Arg Ile Gly Lys His Ser Arg Thr
10 420 425 430

Arg Tyr Glu Arg Asn Ile Glu Lys Ile Ser Met Leu Glu Lys Ile Tyr
435 440 445

Ile His Pro Arg Tyr Asn Trp Arg Glu Asn Leu Asp Arg Asp Ile Ala
450 455 460

15 Leu Met Lys Leu Lys Lys Pro Val Ala Phe Ser Asp Tyr Ile His Pro
465 470 475 480

Val Cys Leu Pro Asp Arg Glu Thr Ala Ala Ser Leu Leu Gln Ala Gly
485 490 495

Tyr Lys Gly Arg Val Thr Gly Trp Gly Asn Leu Lys Glu Thr Trp Thr
20 500 505 510

Ala Asn Val Gly Lys Gly Gln Pro Ser Val Leu Gln Val Val Asn Leu
515 520 525

Pro Ile Val Glu Arg Pro Val Cys Lys Asp Ser Thr Arg Ile Arg Ile
530 535 540

210/335

Thr Asp Asn Met Phe Cys Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg
545 550 555 560
Gly Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Phe Val Met Lys Ser
565 570 575
5 Pro Phe Asn Asn Arg Trp Tyr Gln Met Gly Ile Val Ser Trp Gly Glu
580 585 590
Gly Cys Asp Arg Asp Gly Lys Tyr Gly Phe Tyr Thr His Val Phe Arg
595 600 605
Leu Lys Lys Trp Ile Gln Lys Val Ile Asp Gln Phe Gly Glu
10 610 615 620

<210> 68
<211> 530
15 <212> PRT
<213> Homo sapiens
<220>
<221> Pyruvate kinase
<222> (1)..(530)
20 <223> Accession No. as of 29 August 2003: P14618
<400> 68

Ser Lys Pro His Ser Glu Ala Gly Thr Ala Phe Ile Gln Thr Gln Gln

1

5

10

15

211/335

Leu His Ala Ala Met Ala Asp Thr Phe Leu Glu His Met Cys Arg Leu
 20 25 30
 Asp Ile Asp Ser Pro Pro Ile Thr Ala Arg Asn Thr Gly Ile Ile Cys
 35 40 45
 5 Thr Ile Gly Pro Ala Ser Arg Ser Val Glu Thr Leu Lys Glu Met Ile
 50 55 60
 Lys Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr His
 65 70 75 80
 Glu Tyr His Ala Glu Thr Ile Lys Asn Val Arg Thr Ala Thr Glu Ser
 10 85 90 95
 Phe Ala Ser Asp Pro Ile Leu Tyr Arg Pro Val Ala Val Ala Leu Asp
 100 105 110
 Thr Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly Thr
 115 120 125
 15 Ala Glu Val Glu Leu Lys Lys Gly Ala Thr Leu Lys Ile Thr Leu Asp
 130 135 140
 Asn Ala Tyr Met Glu Lys Cys Asp Glu Asn Ile Leu Trp Leu Asp Tyr
 145 150 155 160
 Lys Asn Ile Cys Lys Val Val Glu Val Gly Ser Lys Ile Tyr Val Asp
 165 170 175
 20 Asp Gly Leu Ile Ser Leu Gln Val Lys Gln Lys Gly Ala Asp Phe Leu
 180 185 190
 Val Thr Glu Val Glu Asn Gly Gly Ser Leu Gly Ser Lys Lys Gly Val
 195 200 205

212/335

Asn Leu Pro Gly Ala Ala Val Asp Leu Pro Ala Val Ser Glu Lys Asp
210 215 220

Ile Gln Asp Leu Lys Phe Gly Val Glu Gln Asp Val Asp Met Val Phe
225 230 235 240

5 Ala Ser Phe Ile Arg Lys Ala Ser Asp Val His Glu Val Arg Lys Val
245 250 255

Leu Gly Glu Lys Gly Lys Asn Ile Lys Ile Ile Ser Lys Ile Glu Asn
260 265 270

His Glu Gly Val Arg Arg Phe Asp Glu Ile Leu Glu Ala Ser Asp Gly
10 275 280 285

Ile Met Val Ala Arg Gly Asp Leu Gly Ile Glu Ile Pro Ala Glu Lys
290 295 300

Val Phe Leu Ala Gln Lys Met Met Ile Gly Arg Cys Asn Arg Ala Gly
305 310 315 320

15 Lys Pro Val Ile Cys Ala Thr Gln Met Leu Glu Ser Met Ile Lys Lys
325 330 335

Pro Arg Pro Thr Arg Ala Glu Gly Ser Asp Val Ala Asn Ala Val Leu
340 345 350

Asp Gly Ala Asp Cys Ile Met Leu Ser Gly Glu Thr Ala Lys Gly Asp
20 355 360 365

Tyr Pro Leu Glu Ala Val Arg Met Gln His Leu Ile Ala Arg Glu Ala
370 375 380

Glu Ala Ala Ile Tyr His Leu Gln Leu Phe Glu Glu Leu Arg Arg Leu
385 390 395 400

213/335

Ala Pro Ile Thr Ser Asp Pro Thr Glu Ala Thr Ala Val Gly Ala Val
405 410 415

Glu Ala Ser Phe Lys Cys Cys Ser Gly Ala Ile Ile Val Leu Thr Lys
420 425 430

5 Ser Gly Arg Ser Ala His Gln Val Ala Arg Tyr Arg Pro Arg Ala Pro
435 440 445

Ile Ile Ala Val Thr Arg Asn Pro Gln Thr Ala Arg Gln Ala His Leu
450 455 460

Tyr Arg Gly Ile Phe Pro Val Leu Cys Lys Asp Pro Val Gln Glu Ala
10 465 470 475 480

Trp Ala Glu Asp Val Asp Leu Arg Val Asn Phe Ala Met Asn Val Gly
485 490 495

Lys Ala Arg Gly Phe Phe Lys Lys Gly Asp Val Val Ile Val Leu Thr
500 505 510

15 Gly Trp Arg Pro Gly Ser Gly Phe Thr Asn Thr Met Arg Val Val Pro
515 520 525

Val Pro
530

20

<210> 69

<211> 328

<212> PRT

<213> Homo sapiens

<220>

<221> Reticulocalbin 3 precursor

<222> (1)..(328)

<223> Accession No. as of 29 August 2003: Q96D15

5 <400> 69

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His
1 5 10 15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly
10 20 25 30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala
35 40 45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
50 55 60
15 Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu
65 70 75 80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
85 90 95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg
20 100 105 110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
115 120 125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
130 135 140

215/335

His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
145 150 155 160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp
165 170 175
5 Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
180 185 190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
195 200 205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
10 210 215 220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
225 230 235 240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
245 250 255
15 Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
260 265 270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
275 280 285
Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
20 290 295 300
Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
305 310 315 320
Leu Thr Arg His His Asp Glu Leu

325

<210> 70
<211> 469
5 <212> PRT
<213> Homo sapiens
<220>
<221> Desmin
<222> (1)..(469)
10 <223> Accession No. as of 29 August 2003: P17661
<400> 70

Ser Gln Ala Tyr Ser Ser Ser Gln Arg Val Ser Ser Tyr Arg Arg Thr
1 5 10 15
15 Phe Gly Gly Ala Pro Gly Phe Pro Leu Gly Ser Pro Leu Ser Ser Pro
20 25 30
Val Phe Pro Arg Ala Gly Phe Gly Ser Lys Gly Ser Ser Ser Ser Val
35 40 45
Thr Ser Arg Val Tyr Gln Val Ser Arg Thr Ser Gly Gly Ala Gly Gly
20 50 55 60
Leu Gly Ser Leu Arg Ala Ser Arg Leu Gly Thr Thr Arg Thr Pro Ser
65 70 75 80
Ser Tyr Gly Ala Gly Glu Leu Leu Asp Phe Ser Leu Ala Asp Ala Val
85 90 95

217/335

Asn Gln Glu Phe Leu Thr Thr Arg Thr Asn Glu Lys Val Glu Leu Gln
100 105 110

Glu Leu Asn Asp Arg Phe Ala Asn Tyr Ile Glu Lys Val Arg Phe Leu
115 120 125

5 Glu Gln Gln Asn Ala Ala Leu Ala Ala Glu Val Asn Arg Leu Lys Gly
130 135 140

Arg Glu Pro Thr Arg Val Ala Glu Leu Tyr Glu Glu Glu Leu Arg Glu
145 150 155 160

Leu Arg Arg Gln Val Glu Val Leu Thr Asn Gln Arg Ala Arg Val Asp
10 165 170 175

Val Glu Arg Asp Asn Leu Leu Asp Asp Leu Gln Arg Leu Lys Ala Lys
180 185 190

Leu Gln Glu Glu Ile Gln Leu Lys Glu Glu Ala Glu Asn Asn Leu Ala
195 200 205

15 Ala Phe Arg Ala Asp Val Asp Ala Ala Thr Leu Ala Arg Ile Asp Leu
210 215 220

Glu Arg Arg Ile Glu Ser Leu Asn Glu Glu Ile Ala Phe Leu Lys Lys
225 230 235 240

Val His Glu Glu Glu Ile Arg Glu Leu Gln Ala Gln Leu Gln Glu Gln
20 245 250 255

Gln Val Gln Val Glu Met Asp Met Ser Lys Pro Asp Leu Thr Ala Ala
260 265 270

Leu Arg Asp Ile Arg Ala Gln Tyr Glu Thr Ile Ala Ala Lys Asn Ile
275 280 285

218/335

Ser Glu Ala Glu Glu Trp Tyr Lys Ser Lys Val Ser Asp Leu Thr Gln
290 295 300
Ala Ala Asn Lys Asn Asn Asp Ala Leu Arg Gln Ala Lys Gln Glu Met
305 310 315 320
5 Met Glu Tyr Arg His Gln Ile Gln Ser Tyr Thr Cys Glu Ile Asp Ala
325 330 335
Leu Lys Gly Thr Asn Asp Ser Leu Met Arg Gln Met Arg Glu Leu Glu
340 345 350
Asp Arg Phe Ala Ser Glu Ala Ser Gly Tyr Gln Asp Asn Ile Ala Arg
10 355 360 365
Leu Glu Glu Glu Ile Arg His Leu Lys Asp Glu Met Ala Arg His Leu
370 375 380
Arg Glu Tyr Gln Asp Leu Leu Asn Val Lys Met Ala Leu Asp Val Glu
385 390 395 400
15 Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser Arg Ile Asn
405 410 415
Leu Pro Ile Gln Thr Tyr Ser Ala Leu Asn Phe Arg Glu Thr Ser Pro
420 425 430
Glu Gln Arg Gly Ser Glu Val His Thr Lys Lys Thr Val Met Ile Lys
20 435 440 445
Thr Ile Glu Thr Arg Asp Gly Glu Val Val Ser Glu Ala Thr Gln Gln
450 455 460
Gln His Glu Val Leu
465

<210> 71
<211> 417
5 <212> PRT
<213> Homo sapiens
<220>
<221> Carboxypeptidase B precursor
<222> (1)..(417)
10 <223> Accession No. as of 29 August 2003: P15086
<400> 71

Met Leu Ala Leu Leu Val Leu Val Thr Val Ala Leu Ala Ser Ala His
1 5 10 15
15 His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn Val
20 25 30
Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr Thr
35 40 45
Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro His
20 50 55 60
Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val Glu
65 70 75 80
Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser Asn
85 90 95

220/335

Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr
100 105 110
Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp
115 120 125
5 Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile Ser Arg Ser Val
130 135 140
Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly
145 150 155 160
Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe His
10 165 170 175
Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp Phe Val Arg Glu
180 185 190
Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr Glu Leu Leu Asp
195 200 205
15 Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile Asp Gly Tyr Ile
210 215 220
Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr Arg Ser Thr His
225 230 235 240
Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg Asn Phe Asp Ala
20 245 250 255
Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys Asp Glu Thr Tyr
260 265 270
Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys Ala Leu Ala Asp
275 280 285

221/335

Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr Leu Thr Ile His
290 295 300
Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr Ala Tyr Lys Leu
305 310 315 320
5 Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys Ala Thr Val Lys
325 330 335
Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr Gly Pro Gly Ala
340 345 350
Thr Thr Ile Tyr Pro Ala Ala Gly Gly Ser Asp Asp Trp Ala Tyr Asp
10 355 360 365
Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr Gly Arg
370 375 380
Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala Thr Cys Glu Glu
385 390 395 400
15 Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val Leu Glu His Leu
405 410 415
Tyr

20

<210> 72

<211> 419

<212> PRT

<213> Homo sapiens

222/335

<220>

<221> Carboxypeptidase A1 precursor

<222> (1)..(419)

<223> Accession No. as of 29 August 2003: P15085

5 <400> 72

Met Arg Gly Leu Leu Val Leu Ser Val Leu Leu Gly Ala Val Phe Gly

1 5 10 15

Lys Glu Asp Phe Val Gly His Gln Val Leu Arg Ile Ser Val Ala Asp

10 20 25 30

Glu Ala Gln Val Gln Lys Val Lys Glu Leu Glu Asp Leu Glu His Leu

35 40 45

Gln Leu Asp Phe Trp Arg Gly Pro Ala His Pro Gly Ser Pro Ile Asp

50 55 60

15 Val Arg Val Pro Phe Pro Ser Ile Gln Ala Val Lys Ile Phe Leu Glu

65 70 75 80

Ser His Gly Ile Ser Tyr Glu Thr Met Ile Glu Asp Val Gln Ser Leu

85 90 95

Leu Asp Glu Glu Gln Glu Gln Met Phe Ala Phe Arg Ser Arg Ala Arg

20 100 105 110

Ser Thr Asp Thr Phe Asn Tyr Ala Thr Tyr His Thr Leu Glu Glu Ile

115 120 125

Tyr Asp Phe Leu Asp Leu Leu Val Ala Glu Asn Pro His Leu Val Ser

130 135 140

223/335

Lys Ile Gln Ile Gly Asn Thr Tyr Glu Gly Arg Pro Ile Tyr Val Leu
145 150 155 160

Lys Phe Ser Thr Gly Gly Ser Lys Arg Pro Ala Ile Trp Ile Asp Thr
165 170 175

5 Gly Ile His Ser Arg Glu Trp Val Thr Gln Ala Ser Gly Val Trp Phe
180 185 190

Ala Lys Lys Ile Thr Gln Asp Tyr Gly Gln Asp Ala Ala Phe Thr Ala
195 200 205

Ile Leu Asp Thr Leu Asp Ile Phe Leu Glu Ile Val Thr Asn Pro Asp
10 210 215 220

Gly Phe Ala Phe Thr His Ser Thr Asn Arg Met Trp Arg Lys Thr Arg
225 230 235 240

Ser His Thr Ala Gly Ser Leu Cys Ile Gly Val Asp Pro Asn Arg Asn
245 250 255

15 Trp Asp Ala Gly Phe Gly Leu Ser Gly Ala Ser Ser Asn Pro Cys Ser
260 265 270

Glu Thr Tyr His Gly Lys Phe Ala Asn Ser Glu Val Glu Val Lys Ser
275 280 285

Ile Val Asp Phe Val Lys Asp His Gly Asn Ile Lys Ala Phe Ile Ser
20 290 295 300

Ile His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr Lys Thr
305 310 315 320

Glu Pro Val Pro Asp Gln Asp Glu Leu Asp Gln Leu Ser Lys Ala Ala
325 330 335

224/335

Val Thr Ala Leu Ala Ser Leu Tyr Gly Thr Lys Phe Asn Tyr Gly Ser
340 345 350
Ile Ile Lys Ala Ile Tyr Gln Ala Ser Gly Ser Thr Ile Asp Trp Thr
355 360 365
5 Tyr Ser Gln Gly Ile Lys Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr
370 375 380
Gly Arg Tyr Gly Phe Leu Leu Pro Ala Ser Gln Ile Ile Pro Thr Ala
385 390 395 400
Lys Glu Thr Trp Leu Ala Leu Leu Thr Ile Met Glu His Thr Leu Asn
10 405 410 415
His Pro Tyr

15 <210> 73

<211> 418

<212> PRT

<213> Homo sapiens

<220>

20 <221> Colligin 2

<222> (1)..(418)

<223> Accession No. as of 29 August 2003: P50454

<400> 73

225/335

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
1 5 10 15
Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr
20 25 30
5 Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala
35 40 45
Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val
50 55 60
Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu
10 65 70 75 80
Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val
85 90 95
Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly
100 105 110
15 Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp
115 120 125
Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp
130 135 140
Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys
20 145 150 155 160
Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp
165 170 175
Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val
180 185 190

226/335

Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro
195 200 205

His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe
210 215 220

5 Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr
225 230 235 240

Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val
245 250 255

Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro
10 260 265 270

His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu
275 280 285

Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile
290 295 300

15 Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His
305 310 315 320

Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp
325 330 335

Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe
20 340 345 350

His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln
355 360 365

Asp Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala
370 375 380

227/335

Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu

385

390

395

400

Leu Phe Ile Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp

405

410

415

5 Glu Leu

<210> 74

10 <211> 263

<212> PRT

<213> Homo sapiens

<220>

<221> Chymotrypsinogen B precursor

15 <222> (1)..(263)

<223> Accession No. as of 29 August 2003: P17538

<400> 74

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr

20 1

5

10

15

Phe Gly Cys Gly Val Pro Ala Ile His Pro Val Leu Ser Gly Leu Ser

20

25

30

Arg Ile Val Asn Gly Glu Asp Ala Val Pro Gly Ser Trp Pro Trp Gln

35

40

45

228/335

Val Ser Leu Gln Asp Lys Thr Gly Phe His Phe Cys Gly Gly Ser Leu
50 55 60

Ile Ser Glu Asp Trp Val Val Thr Ala Ala His Cys Gly Val Arg Thr
65 70 75 80

5 Ser Asp Val Val Val Ala Gly Glu Phe Asp Gln Gly Ser Asp Glu Glu
85 90 95

Asn Ile Gln Val Leu Lys Ile Ala Lys Val Phe Lys Asn Pro Lys Phe
100 105 110

Ser Ile Leu Thr Val Asn Asn Asp Ile Thr Leu Leu Lys Leu Ala Thr
10 115 120 125

Pro Ala Arg Phe Ser Gln Thr Val Ser Ala Val Cys Leu Pro Ser Ala
130 135 140

Asp Asp Asp Phe Pro Ala Gly Thr Leu Cys Ala Thr Thr Gly Trp Gly
145 150 155 160

15 Lys Thr Lys Tyr Asn Ala Asn Lys Thr Pro Asp Lys Leu Gln Gln Ala
165 170 175

Ala Leu Pro Leu Leu Ser Asn Ala Glu Cys Lys Lys Ser Trp Gly Arg
180 185 190

Arg Ile Thr Asp Val Met Ile Cys Ala Gly Ala Ser Gly Val Ser Ser
20 195 200 205

Cys Met Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Asp Gly Ala
210 215 220

Trp Thr Leu Val Gly Ile Val Ser Trp Gly Ser Asp Thr Cys Ser Thr
225 230 235 240

229/335

Ser Ser Pro Gly Val Tyr Ala Arg Val Thr Lys Leu Ile Pro Trp Val

245

250

255

Gln Lys Ile Leu Ala Ala Asn

260

5

<210> 75

<211> 247

<212> PRT

10 <213> Homo sapiens

<220>

<221> Trypsin I precursor

<222> (1)..(247)

<223> Accession No. as of 29 August 2003: P07477

15 <400> 75

Met Asn Pro Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Leu Ala Ala

1

5

10

15

Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Glu Glu

20

20

25

30

Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys

35

40

45

Gly Gly Ser Leu Ile Asn Glu Gln Trp Val Val Ser Ala Gly His Cys

50

55

60

230/335

Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val
65 70 75 80
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His
85 90 95
5 Pro Gln Tyr Asp Arg Lys Thr Leu Asn Asn Asp Ile Met Leu Ile Lys
100 105 110
Leu Ser Ser Arg Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu
115 120 125
Pro Thr Ala Pro Pro Ala Thr Gly Thr Lys Cys Leu Ile Ser Gly Trp
10 130 135 140
Gly Asn Thr Ala Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys
145 150 155 160
Leu Asp Ala Pro Val Leu Ser Gln Ala Lys Cys Glu Ala Ser Tyr Pro
165 170 175
15 Gly Lys Ile Thr Ser Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly
180 185 190
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly
195 200 205
Gln Leu Gln Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Lys Asn
20 210 215 220
Lys Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Lys Trp Ile Lys
225 230 235 240
Asn Thr Ile Ala Ala Asn Ser

245

<210> 76
<211> 247
5 <212> PRT
<213> Homo sapiens
<220>
<221> Trypsin II precursor
<222> (1)..(247)
10 <223> Accession No. as of 29 August 2003: P07478
<400> 76

Met Asn Leu Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Val Ala Ala
1 5 10 15
15 Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Ile Cys Glu Glu
20 25 30
Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys
35 40 45
Gly Gly Ser Leu Ile Ser Glu Gln Trp Val Val Ser Ala Gly His Cys
20 50 55 60
Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val
65 70 75 80
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His
85 90 95

232/335

Pro Lys Tyr Asn Ser Arg Thr Leu Asp Asn Asp Ile Leu Leu Ile Lys
100 105 110
Leu Ser Ser Pro Ala Val Ile Asn Ser Arg Val Ser Ala Ile Ser Leu
115 120 125
5 Pro Thr Ala Pro Pro Ala Ala Gly Thr Glu Ser Leu Ile Ser Gly Trp
130 135 140
Gly Asn Thr Leu Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys
145 150 155 160
Leu Asp Ala Pro Val Leu Ser Gln Ala Glu Cys Glu Ala Ser Tyr Pro
10 165 170 175
Gly Lys Ile Thr Asn Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly
180 185 190
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Ser Asn Gly
195 200 205
15 Glu Leu Gln Gly Ile Val Ser Trp Gly Tyr Gly Cys Ala Gln Lys Asn
210 215 220
Arg Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Asp Trp Ile Lys
225 230 235 240
Asp Thr Ile Ala Ala Asn Ser
20 245

<210> 77

<211> 379

233/335

<212> PRT

<213> Homo sapiens

<220>

<221> Leukocyte elastase inhibitor (LEI)

5 <222> (1)..(379)

<223> Accession No. as of 29 August 2003: P30740

<400> 77

Met Glu Gln Leu Ser Ser Ala Asn Thr Arg Phe Ala Leu Asp Leu Phe
10 1 5 10 15
Leu Ala Leu Ser Glu Asn Asn Pro Ala Gly Asn Ile Phe Ile Ser Pro
20 25 30
Phe Ser Ile Ser Ser Ala Met Ala Met Val Phe Leu Gly Thr Arg Gly
35 40 45
15 Asn Thr Ala Ala Gln Leu Ser Lys Thr Phe His Phe Asn Thr Val Glu
50 55 60
Glu Val His Ser Arg Phe Gln Ser Leu Asn Ala Asp Ile Asn Lys Arg
65 70 75 80
Gly Ala Ser Tyr Ile Leu Lys Leu Ala Asn Arg Leu Tyr Gly Glu Lys
20 85 90 95
Thr Tyr Asn Phe Leu Pro Glu Phe Leu Val Ser Thr Gln Lys Thr Tyr
100 105 110
Gly Ala Asp Leu Ala Ser Val Asp Phe Gln His Ala Ser Glu Asp Ala
115 120 125

234/335

Arg Lys Thr Ile Asn Gln Trp Val Lys Gly Gln Thr Glu Gly Lys Ile
130 135 140

Pro Glu Leu Leu Ala Ser Gly Met Val Asp Asn Met Thr Lys Leu Val
145 150 155 160

5 Leu Val Asn Ala Ile Tyr Phe Lys Gly Asn Trp Lys Asp Lys Phe Met
165 170 175

Lys Glu Ala Thr Thr Asn Ala Pro Phe Arg Leu Asn Lys Lys Asp Arg
180 185 190

Lys Thr Val Lys Met Met Tyr Gln Lys Lys Lys Phe Ala Tyr Gly Tyr
10 195 200 205

Ile Glu Asp Leu Lys Cys Arg Val Leu Glu Leu Pro Tyr Gln Gly Glu
210 215 220

Glu Leu Ser Met Val Ile Leu Leu Pro Asp Asp Ile Glu Asp Glu Ser
225 230 235 240

15 Thr Gly Leu Lys Lys Ile Glu Glu Gln Leu Thr Leu Glu Lys Leu His
245 250 255

Glu Trp Thr Lys Pro Glu Asn Leu Asp Phe Ile Glu Val Asn Val Ser
260 265 270

Leu Pro Arg Phe Lys Leu Glu Glu Ser Tyr Thr Leu Asn Ser Asp Leu
20 275 280 285

Ala Arg Leu Gly Val Gln Asp Leu Phe Asn Ser Ser Lys Ala Asp Leu
290 295 300

Ser Gly Met Ser Gly Ala Arg Asp Ile Phe Ile Ser Lys Ile Val His
305 310 315 320

235/335

Lys Ser Phe Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala

325

330

335

Thr Ala Gly Ile Ala Thr Phe Cys Met Leu Met Pro Glu Glu Asn Phe

340

345

350

5 Thr Ala Asp His Pro Phe Leu Phe Phe Ile Arg His Asn Ser Ser Gly

355

360

365

Ser Ile Leu Phe Leu Gly Arg Phe Ser Ser Pro

370

375

10

<210> 78

<211> 573

<212> PRT

<213> Homo sapiens

15 <220>

<221> Hsp60

<222> (1)..(573)

<223> Accession No. as of 29 August 2003: P10809

<400> 78

20

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg

1

5

10

15

Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe

20

25

30

236/335

Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
35 40 45

Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile
50 55 60

5 Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val
65 70 75 80

Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
85 90 95

Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly
10 100 105 110

Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe
115 120 125

Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
130 135 140

15 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
145 150 155 160

Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala
165 170 175

Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
20 180 185 190

Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
195 200 205

Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
210 215 220

237/335

Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
225 230 235 240

Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
245 250 255

5 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val
260 265 270

Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
275 280 285

Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
10 290 295 300

Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
305 310 315 320

Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
325 330 335

15 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
340 345 350

Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu
355 360 365

Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu
20 370 375 380

Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly
385 390 395 400

Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
405 410 415

238/335

Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
420 425 430
Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile
435 440 445
5 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
450 455 460
Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
465 470 475 480
Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
10 485 490 495
Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
500 505 510
Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
515 520 525
15 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
530 535 540
Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
545 550 555 560
Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
20 565 570

<210> 79

<211> 803

239/335

<212> PRT

<213> Homo sapiens

<220>

<221> Endoplasmin precursor (GRP94)

5 <222> (1)..(803)

<223> Accession No. as of 29 August 2003: P14625

<400> 79

Met Arg Ala Leu Trp Val Leu Gly Leu Cys Cys Val Leu Leu Thr Phe
10 1 5 10 15
Gly Ser Val Arg Ala Asp Asp Glu Val Asp Val Asp Gly Thr Val Glu
20 25 30
Glu Asp Leu Gly Lys Ser Arg Glu Gly Ser Arg Thr Asp Asp Glu Val
35 40 45
15 Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala Ser
50 55 60
Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln Ala
65 70 75 80
Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys Asn
20 85 90 95
Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu
100 105 110
Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ser Gly
115 120 125

240/335

Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn Leu
130 135 140

Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Glu Leu Val
145 150 155 160

5 Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu Asn
165 170 175

Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile
180 185 190

Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys
10 195 200 205

Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln His Ile Trp Glu
210 215 220

Ser Asp Ser Asn Glu Phe Ser Val Ile Ala Asp Pro Arg Gly Asn Thr
225 230 235 240

15 Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys Glu Glu Ala Ser
245 250 255

Asp Tyr Leu Glu Leu Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr Ser
260 265 270

Gln Phe Ile Asn Phe Pro Ile Tyr Val Trp Ser Ser Lys Thr Glu Thr
20 275 280 285

Val Glu Glu Pro Met Glu Glu Glu Glu Ala Ala Lys Glu Glu Lys Glu
290 295 300

Glu Ser Asp Asp Glu Ala Ala Val Glu Glu Glu Glu Glu Glu Lys Lys
305 310 315 320

241/335

Pro Lys Thr Lys Lys Val Glu Lys Thr Val Trp Asp Trp Glu Leu Met
325 330 335

Asn Asp Ile Lys Pro Ile Trp Gln Arg Pro Ser Lys Glu Val Glu Glu
340 345 350

5 Asp Glu Tyr Lys Ala Phe Tyr Lys Ser Phe Ser Lys Glu Ser Asp Asp
355 360 365

Pro Met Ala Tyr Ile His Phe Thr Ala Glu Gly Glu Val Thr Phe Lys
370 375 380

Ser Ile Leu Phe Val Pro Thr Ser Ala Pro Arg Gly Leu Phe Asp Glu
10 385 390 395 400

Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr Val Arg Arg Val
405 410 415

Phe Ile Thr Asp Asp Phe His Asp Met Met Pro Lys Tyr Leu Asn Phe
420 425 430

15 Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Val Ser Arg
435 440 445

Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val Ile Arg Lys Lys Leu
450 455 460

Val Arg Lys Thr Leu Asp Met Ile Lys Lys Ile Ala Asp Asp Lys Tyr
20 465 470 475 480

Asn Asp Thr Phe Trp Lys Glu Phe Gly Thr Asn Ile Lys Leu Gly Val
485 490 495

Ile Glu Asp His Ser Asn Arg Thr Arg Leu Ala Lys Leu Leu Arg Phe
500 505 510

242/335

Gln Ser Ser His His Pro Thr Asp Ile Thr Ser Leu Asp Gln Tyr Val
515 520 525

Glu Arg Met Lys Glu Lys Gln Asp Lys Ile Tyr Phe Met Ala Gly Ser
530 535 540

5 Ser Arg Lys Glu Ala Glu Ser Ser Pro Phe Val Glu Arg Leu Leu Lys
545 550 555 560

Lys Gly Tyr Glu Val Ile Tyr Leu Thr Glu Pro Val Asp Glu Tyr Cys
565 570 575

Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val Ala
10 580 585 590

Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser Arg
595 600 605

Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys Asp
610 615 620

15 Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg Leu
625 630 635 640

Thr Glu Ser Pro Cys Ala Leu Val Ala Ser Gln Tyr Gly Trp Ser Gly
645 650 655

Asn Met Glu Arg Ile Met Lys Ala Gln Ala Tyr Gln Thr Gly Lys Asp
20 660 665 670

Ile Ser Thr Asn Tyr Tyr Ala Ser Gln Lys Lys Thr Phe Glu Ile Asn
675 680 685

Pro Arg His Pro Leu Ile Arg Asp Met Leu Arg Arg Ile Lys Glu Asp
690 695 700

243/335

Glu Asp Asp Lys Thr Val Leu Asp Leu Ala Val Val Leu Phe Glu Thr
705 710 715 720
Ala Thr Leu Arg Ser Gly Tyr Leu Leu Pro Asp Thr Lys Ala Tyr Gly
725 730 735
5 Asp Arg Ile Glu Arg Met Leu Arg Leu Ser Leu Asn Ile Asp Pro Asp
740 745 750
Ala Lys Val Glu Glu Glu Pro Glu Glu Glu Pro Glu Glu Thr Ala Glu
755 760 765
Asp Thr Thr Glu Asp Thr Glu Gln Asp Glu Asp Glu Glu Met Asp Val
10 770 775 780
Gly Thr Asp Glu Glu Glu Glu Thr Ala Lys Glu Ser Thr Ala Glu Lys
785 790 795 800
Asp Glu Leu
15

<210> 80

<211> 261

<212> PRT
20 <213> Homo sapiens

<220>

<221> Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28)

<222> (1)..(261)

<223> Accession No. as of 29 August 2003: P30040

244/335

<400> 80

Met Ala Ala Ala Val Pro Arg Ala Ala Phe Leu Ser Pro Leu Leu Pro
1 5 10 15
5 Leu Leu Leu Gly Phe Leu Leu Leu Ser Ala Pro His Gly Gly Ser Gly
20 25 30
Leu His Thr Lys Gly Ala Leu Pro Leu Asp Thr Val Thr Phe Tyr Lys
35 40 45
Val Ile Pro Lys Ser Lys Phe Val Leu Val Lys Phe Asp Thr Gln Tyr
10 50 55 60
Pro Tyr Gly Glu Lys Gln Asp Glu Phe Lys Arg Leu Ala Glu Asn Ser
65 70 75 80
Ala Ser Ser Asp Asp Leu Leu Val Ala Glu Val Gly Ile Ser Asp Tyr
85 90 95
15 Gly Asp Lys Leu Asn Met Glu Leu Ser Glu Lys Tyr Lys Leu Asp Lys
100 105 110
Glu Ser Tyr Pro Val Phe Tyr Leu Phe Arg Asp Gly Asp Phe Glu Asn
115 120 125
Pro Val Pro Tyr Thr Gly Ala Val Lys Val Gly Ala Ile Gln Arg Trp
20 130 135 140
Leu Lys Gly Gln Gly Val Tyr Leu Gly Met Pro Gly Cys Leu Pro Val
145 150 155 160
Tyr Asp Ala Leu Ala Gly Glu Phe Ile Arg Ala Ser Gly Val Glu Ala
165 170 175

245/335

Arg Gln Ala Leu Leu Lys Gln Gly Gln Asp Asn Leu Ser Ser Val Lys
180 185 190
Glu Thr Gln Lys Lys Trp Ala Glu Gln Tyr Leu Lys Ile Met Gly Lys
195 200 205
5 Ile Leu Asp Gln Gly Glu Asp Phe Pro Ala Ser Glu Met Thr Arg Ile
210 215 220
Ala Arg Leu Ile Glu Lys Asn Lys Met Ser Asp Gly Lys Lys Glu Glu
225 230 235 240
Leu Gln Lys Ser Leu Asn Ile Leu Thr Ala Phe Gln Lys Lys Gly Ala
10 245 250 255
Glu Lys Glu Glu Leu
260

15 <210> 81

<211> 525

<212> PRT

<213> Homo sapiens

<220>

20 <221> Protein disulfide isomerase A2 precursor

<222> (1)..(525)

<223> Accession No. as of 29 August 2003: Q13087

<400> 81

246/335

Met Ser Arg Gln Leu Leu Pro Val Leu Leu Leu Leu Leu Arg Ala
 1 5 10 15
 Ser Cys Pro Trp Gly Gln Glu Gln Gly Ala Arg Ser Pro Ser Glu Glu
 20 25 30
 5 Pro Pro Glu Glu Glu Ile Pro Lys Glu Asp Gly Ile Leu Val Leu Ser
 35 40 45
 Arg His Thr Leu Gly Leu Ala Leu Arg Glu His Pro Ala Leu Leu Val
 50 55 60
 Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala Pro Glu
 10 65 70 75 80
 Tyr Ser Lys Ala Ala Ala Val Leu Ala Ala Glu Ser Met Val Val Thr
 85 90 95
 Leu Ala Lys Val Asp Gly Pro Ala Gln Arg Glu Leu Ala Glu Glu Phe
 100 105 110
 15 Gly Val Thr Glu Tyr Pro Thr Leu Lys Phe Phe Arg Asn Gly Asn Arg
 115 120 125
 Thr His Pro Glu Glu Tyr Thr Gly Pro Arg Asp Ala Glu Gly Ile Ala
 130 135 140
 Glu Trp Leu Arg Arg Arg Val Gly Pro Ser Ala Met Arg Leu Glu Asp
 20 145 150 155 160
 Glu Ala Ala Ala Gln Ala Leu Ile Gly Gly Arg Asp Leu Val Val Ile
 165 170 175
 Gly Phe Phe Gln Asp Leu Gln Asp Glu Asp Val Ala Thr Phe Leu Ala
 180 185 190

247/335

Leu Ala Gln Asp Ala Leu Asp Met Thr Phe Gly Leu Thr Asp Arg Pro
195 200 205

Arg Leu Phe Gln Gln Phe Gly Leu Thr Lys Asp Thr Val Val Leu Phe
210 215 220

5 Lys Lys Phe Asp Glu Gly Arg Ala Asp Phe Pro Val Asp Glu Glu Leu
225 230 235 240

Gly Leu Asp Leu Gly Asp Leu Ser Arg Phe Leu Val Thr His Ser Met
245 250 255

Arg Leu Val Thr Glu Phe Asn Ser Gln Thr Ser Ala Lys Ile Phe Ala
10 260 265 270

Ala Arg Ile Leu Asn His Leu Leu Leu Phe Val Asn Gln Thr Leu Ala
275 280 285

Ala His Arg Glu Leu Leu Ala Gly Phe Gly Glu Ala Ala Pro Arg Phe
290 295 300

15 Arg Gly Gln Val Leu Phe Val Val Val Asp Val Ala Ala Asp Asn Glu
305 310 315 320

His Val Leu Gln Tyr Phe Gly Leu Lys Ala Glu Ala Ala Pro Thr Leu
325 330 335

Arg Leu Val Asn Leu Glu Thr Thr Lys Lys Tyr Ala Pro Val Asp Gly
20 340 345 350

Gly Pro Val Thr Ala Ala Ser Ile Thr Ala Phe Cys His Ala Val Leu
355 360 365

Asn Gly Gln Val Lys Pro Tyr Leu Leu Ser Gln Glu Ile Pro Pro Asp
370 375 380

248/335

Trp Asp Gln Arg Pro Val Lys Thr Leu Val Gly Lys Asn Phe Glu Gln
385 390 395 400
Val Ala Phe Asp Glu Thr Lys Asn Val Phe Val Lys Phe Tyr Ala Pro
405 410 415
5 Trp Cys Thr His Cys Lys Glu Met Ala Pro Ala Trp Glu Ala Leu Ala
420 425 430
Glu Lys Tyr Gln Asp His Glu Asp Ile Ile Ile Ala Glu Leu Asp Ala
435 440 445
Thr Ala Asn Glu Leu Asp Ala Phe Ala Val His Gly Phe Pro Thr Leu
10 450 455 460
Lys Tyr Phe Pro Ala Gly Pro Gly Arg Lys Val Ile Glu Tyr Lys Ser
465 470 475 480
Thr Arg Asp Leu Glu Thr Phe Ser Lys Phe Leu Asp Asn Gly Gly Val
485 490 495
15 Leu Pro Thr Glu Glu Pro Pro Glu Glu Pro Ala Ala Pro Phe Pro Glu
500 505 510
Pro Pro Ala Asn Ser Thr Met Gly Ser Lys Glu Glu Leu
515 520 525
20
<210> 82
<211> 505
<212> PRT
<213> Homo sapiens

<220>

<221> Protein disulfide isomerase A3 precursor

<222> (1)..(505)

<223> Accession No. as of 29 August 2003: P30101

5 <400> 82

Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu
1 5 10 15
Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp
10 20 25 30
Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met
35 40 45
Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala
50 55 60
15 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu
65 70 75 80
Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly
85 90 95
Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala
10 100 105 110
Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu
115 120 125
Lys Lys Gln Ala Gly Pro Ala Ser Val Pro Leu Arg Thr Glu Glu Glu
130 135 140

250/335

Phe Lys Lys Phe Ile Ser Asp Lys Asp Ala Ser Ile Val Gly Phe Phe
145 150 155 160
Asp Asp Ser Phe Ser Glu Ala His Ser Glu Phe Leu Lys Ala Ala Ser
165 170 175
5 Asn Leu Arg Asp Asn Tyr Arg Phe Ala His Thr Asn Val Glu Ser Leu
180 185 190
Val Asn Glu Tyr Asp Asp Asn Gly Glu Gly Ile Ile Leu Phe Arg Pro
195 200 205
Ser His Leu Thr Asn Lys Phe Glu Asp Lys Thr Val Ala Tyr Thr Glu
10 210 215 220
Gln Lys Met Thr Ser Gly Lys Ile Lys Lys Phe Ile Gln Glu Asn Ile
225 230 235 240
Phe Gly Ile Cys Pro His Met Thr Glu Asp Asn Lys Asp Leu Ile Gln
245 250 255
15 Gly Lys Asp Leu Leu Ile Ala Tyr Tyr Asp Val Asp Tyr Glu Lys Asn
260 265 270
Ala Lys Gly Ser Asn Tyr Trp Arg Asn Arg Val Met Met Val Ala Lys
275 280 285
Lys Phe Leu Asp Ala Gly His Lys Leu Asn Phe Ala Val Ala Ser Arg
20 290 295 300
Lys Thr Phe Ser His Glu Leu Ser Asp Phe Gly Leu Glu Ser Thr Ala
305 310 315 320
Gly Glu Ile Pro Val Val Ala Ile Arg Thr Ala Lys Gly Glu Lys Phe
325 330 335

251/335

Val Met Gln Glu Glu Phe Ser Arg Asp Gly Lys Ala Leu Glu Arg Phe
340 345 350

Leu Gln Asp Tyr Phe Asp Gly Asn Leu Lys Arg Tyr Leu Lys Ser Glu
355 360 365

5 Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Val Ala Glu
370 375 380

Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu
385 390 395 400

Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr
10 405 410 415

Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala
420 425 430

Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg
435 440 445

15 Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro
450 455 460

Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu
465 470 475 480

Gln Arg Glu Ala Thr Asn Pro Pro Val Ile Gln Glu Glu Lys Pro Lys
20 485 490 495

Lys Lys Lys Lys Ala Gln Glu Asp Leu
500 505

<210> 83

<211> 374

<212> PRT

<213> Homo sapiens

5 <220>

<221> Alcohol dehydrogenase beta chain

<222> (1)..(374)

<223> Accession No. as of 29 August 2003: P00325

<400> 83

10

Ser Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp Glu

1 5 10 15

Val Lys Lys Pro Phe Ser Ile Glu Asp Val Glu Val Ala Pro Pro Lys

20 25 30

15 Ala Tyr Glu Val Arg Ile Lys Met Val Ala Val Gly Ile Cys Arg Thr

35 40 45

Asp Asp His Val Val Ser Gly Asn Leu Val Thr Pro Leu Pro Val Ile

50 55 60

Leu Gly His Glu Ala Ala Gly Ile Val Glu Ser Val Gly Glu Gly Val

20 65 70 75 80

Thr Thr Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Thr Pro Gln

85 90 95

Cys Gly Lys Cys Arg Val Cys Lys Asn Pro Glu Ser Asn Tyr Cys Leu

100 105 110

253/335

Lys Asn Asp Leu Gly Asn Pro Arg Gly Thr Leu Gln Asp Gly Thr Arg
115 120 125

Arg Phe Thr Cys Arg Gly Lys Pro Ile His His Phe Leu Gly Thr Ser
130 135 140

5 Thr Phe Ser Gln Tyr Thr Val Val Asp Glu Asn Ala Val Ala Lys Ile
145 150 155 160

Asp Ala Ala Ser Pro Leu Glu Lys Val Cys Leu Ile Gly Cys Gly Phe
165 170 175

Ser Thr Gly Tyr Gly Ser Ala Val Asn Val Ala Lys Val Thr Pro Gly
10 180 185 190

Ser Thr Cys Ala Val Phe Gly Leu Gly Gly Val Gly Leu Ser Ala Val
195 200 205

Met Gly Cys Lys Ala Ala Gly Ala Ala Arg Ile Ile Ala Val Asp Ile
210 215 220

15 Asn Lys Asp Lys Phe Ala Lys Ala Lys Glu Leu Gly Ala Thr Glu Cys
225 230 235 240

Ile Asn Pro Gln Asp Tyr Lys Lys Pro Ile Gln Glu Val Leu Lys Glu
245 250 255

Met Thr Asp Gly Gly Val Asp Phe Ser Phe Glu Val Ile Gly Arg Leu
20 260 265 270

Asp Thr Met Met Ala Ser Leu Leu Cys Cys His Glu Ala Cys Gly Thr
275 280 285

Ser Val Ile Val Gly Val Pro Pro Ala Ser Gln Asn Leu Ser Ile Asn
290 295 300

254/335

Pro Met Leu Leu Leu Thr Gly Arg Thr Trp Lys Gly Ala Val Tyr Gly
305 310 315 320
Gly Phe Lys Ser Lys Glu Gly Ile Pro Lys Leu Val Ala Asp Phe Met
325 330 335
5 Ala Lys Lys Phe Ser Leu Asp Ala Leu Ile Thr His Val Leu Pro Phe
340 345 350
Glu Lys Ile Asn Glu Gly Phe Asp Leu Leu His Ser Gly Lys Ser Ile
355 360 365
Arg Thr Val Leu Thr Phe
10 370

<210> 84

<211> 241

15 <212> PRT

<213> Homo sapiens

<220>

<221> Glutathione transferase omega 1

<222> (1)..(241)

20 <223> Accession No. as of 29 August 2003: P78417

<400> 84

Met Ser Gly Glu Ser Ala Arg Ser Leu Gly Lys Gly Ser Ala Pro Pro

1

5

10

15

255/335

Gly Pro Val Pro Glu Gly Ser Ile Arg Ile Tyr Ser Met Arg Phe Cys
20 25 30

Pro Phe Ala Glu Arg Thr Arg Leu Val Leu Lys Ala Lys Gly Ile Arg
35 40 45

5 His Glu Val Ile Asn Ile Asn Leu Lys Asn Lys Pro Glu Trp Phe Phe
50 55 60

Lys Lys Asn Pro Phe Gly Leu Val Pro Val Leu Glu Asn Ser Gln Gly
65 70 75 80

Gln Leu Ile Tyr Glu Ser Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala
10 85 90 95

Tyr Pro Gly Lys Lys Leu Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys
100 105 110

Gln Lys Met Ile Leu Glu Leu Phe Ser Lys Val Pro Ser Leu Val Gly
115 120 125

15 Ser Phe Ile Arg Ser Gln Asn Lys Glu Asp Tyr Ala Gly Leu Lys Glu
130 135 140

Glu Phe Arg Lys Glu Phe Thr Lys Leu Glu Glu Val Leu Thr Asn Lys
145 150 155 160

Lys Thr Thr Phe Phe Gly Gly Asn Ser Ile Ser Met Ile Asp Tyr Leu
20 165 170 175

Ile Trp Pro Trp Phe Glu Arg Leu Glu Ala Met Lys Leu Asn Glu Cys
180 185 190

Val Asp His Thr Pro Lys Leu Lys Leu Trp Met Ala Ala Met Lys Glu
195 200 205

256/335

Asp Pro Thr Val Ser Ala Leu Leu Thr Ser Glu Lys Asp Trp Gln Gly

210

215

220

Phe Leu Glu Leu Tyr Leu Gln Asn Ser Pro Glu Ala Cys Asp Tyr Gly

225

230

235

240

5 Leu

<210> 85

10 <211> 999

<212> PRT

<213> Homo sapiens

<220>

<221> 150 kDa oxygen-regulated protein precursor (Orp150)

15 <222> (1)..(999)

<223> Accession No. as of 29 August 2003: Q9Y4L1

<400> 85

Met Ala Asp Lys Val Arg Arg Gln Arg Pro Arg Arg Arg Val Cys Trp

20 1

5

10

15

Ala Leu Val Ala Val Leu Leu Ala Asp Leu Leu Ala Leu Ser Asp Thr

20

25

30

Leu Ala Val Met Ser Val Asp Leu Gly Ser Glu Ser Met Lys Val Ala

35

40

45

257/335

Ile Val Lys Pro Gly Val Pro Met Glu Ile Val Leu Asn Lys Glu Ser
50 55 60

Arg Arg Lys Thr Pro Val Ile Val Thr Leu Lys Glu Asn Glu Arg Phe
65 70 75 80

5 Phe Gly Asp Ser Ala Ala Ser Met Ala Ile Lys Asn Pro Lys Ala Thr
85 90 95

Leu Arg Tyr Phe Gln His Leu Leu Gly Lys Gln Ala Asp Asn Pro His
100 105 110

Val Ala Leu Tyr Gln Ala Arg Phe Pro Glu His Glu Leu Thr Phe Asp
10 115 120 125

Pro Gln Arg Gln Thr Val His Phe Gln Ile Ser Ser Gln Leu Gln Phe
130 135 140

Ser Pro Glu Glu Val Leu Gly Met Val Leu Asn Tyr Ser Arg Ser Leu
145 150 155 160

15 Ala Glu Asp Phe Ala Glu Gln Pro Ile Lys Asp Ala Val Ile Thr Val
165 170 175

Pro Val Phe Phe Asn Gln Ala Glu Arg Arg Ala Val Leu Gln Ala Ala
180 185 190

Arg Met Ala Gly Leu Lys Val Leu Gln Leu Ile Asn Asp Asn Thr Ala
20 195 200 205

Thr Ala Leu Ser Tyr Gly Val Phe Arg Arg Lys Asp Ile Asn Thr Thr
210 215 220

Ala Gln Asn Ile Met Phe Tyr Asp Met Gly Ser Gly Ser Thr Val Cys
225 230 235 240

258/335

Thr Ile Val Thr Tyr Gln Met Val Lys Thr Lys Glu Ala Gly Met Gln
245 250 255

Pro Gln Leu Gln Ile Arg Gly Val Gly Phe Asp Arg Thr Leu Gly Gly
260 265 270

5 Leu Glu Met Glu Leu Arg Leu Arg Glu Arg Leu Ala Gly Leu Phe Asn
275 280 285

Glu Gln Arg Lys Gly Gln Arg Ala Lys Asp Val Arg Glu Asn Pro Arg
290 295 300

Ala Met Ala Lys Leu Leu Arg Glu Ala Asn Arg Leu Lys Thr Val Leu
10 305 310 315 320

Ser Ala Asn Ala Asp His Met Ala Gln Ile Glu Gly Leu Met Asp Asp
325 330 335

Val Asp Phe Lys Ala Lys Val Thr Arg Val Glu Phe Glu Glu Leu Cys
340 345 350

15 Ala Asp Leu Phe Glu Arg Val Pro Gly Pro Val Gln Gln Ala Leu Gln
355 360 365

Ser Ala Glu Met Ser Leu Asp Glu Ile Glu Gln Val Ile Leu Val Gly
370 375 380

Gly Ala Thr Arg Val Pro Arg Val Gln Glu Val Leu Leu Lys Ala Val
20 385 390 395 400

Gly Lys Glu Glu Leu Gly Lys Asn Ile Asn Ala Asp Glu Ala Ala Ala
405 410 415

Met Gly Ala Val Tyr Gln Ala Ala Ala Leu Ser Lys Ala Phe Lys Val
420 425 430

259/335

Lys Pro Phe Val Val Arg Asp Ala Val Val Tyr Pro Ile Leu Val Glu
435 440 445

Phe Thr Arg Glu Val Glu Glu Glu Pro Gly Ile His Ser Leu Lys His
450 455 460

5 Asn Lys Arg Val Leu Phe Ser Arg Met Gly Pro Tyr Pro Gln Arg Lys
465 470 475 480

Val Ile Thr Phe Asn Arg Tyr Ser His Asp Phe Asn Phe His Ile Asn
485 490 495

Tyr Gly Asp Leu Gly Phe Leu Gly Pro Glu Asp Leu Arg Val Phe Gly
10 500 505 510

Ser Gln Asn Leu Thr Thr Val Lys Leu Lys Gly Val Gly Asp Ser Phe
515 520 525

Lys Lys Tyr Pro Asp Tyr Glu Ser Lys Gly Ile Lys Ala His Phe Asn
530 535 540

15 Leu Asp Glu Ser Gly Val Leu Ser Leu Asp Arg Val Glu Ser Val Phe
545 550 555 560

Glu Thr Leu Val Glu Asp Ser Ala Glu Glu Glu Ser Thr Leu Thr Lys
565 570 575

Leu Gly Asn Thr Ile Ser Ser Leu Phe Gly Gly Gly Thr Thr Pro Asp
20 580 585 590

Ala Lys Glu Asn Gly Thr Asp Thr Val Gln Glu Glu Glu Ser Pro
595 600 605

Ala Glu Gly Ser Lys Asp Glu Pro Gly Glu Gln Val Glu Leu Lys Glu
610 615 620

260/335

Glu Ala Glu Ala Pro Val Glu Asp Gly Ser Gln Pro Pro Pro Pro Glu
625 630 635 640

Pro Lys Gly Asp Ala Thr Pro Glu Gly Glu Lys Ala Thr Glu Lys Glu
645 650 655

5 Asn Gly Asp Lys Ser Glu Ala Gln Lys Pro Ser Glu Lys Ala Glu Ala
660 665 670

Gly Pro Glu Gly Val Ala Pro Ala Pro Glu Gly Glu Lys Lys Gln Lys
675 680 685

Pro Ala Arg Lys Arg Arg Met Val Glu Glu Ile Gly Val Glu Leu Val
10 690 695 700

Val Leu Asp Leu Pro Asp Leu Pro Glu Asp Lys Leu Ala Gln Ser Val
705 710 715 720

Gln Lys Leu Gln Asp Leu Thr Leu Arg Asp Leu Glu Lys Gln Glu Arg
725 730 735

15 Glu Lys Ala Ala Asn Ser Leu Glu Ala Phe Ile Phe Glu Thr Gln Asp
740 745 750

Lys Leu Tyr Gln Pro Glu Tyr Gln Glu Val Ser Thr Glu Glu Gln Arg
755 760 765

Glu Glu Ile Ser Gly Lys Leu Ser Ala Ala Ser Thr Trp Leu Glu Asp
20 770 775 780

Glu Gly Val Gly Ala Thr Thr Val Met Leu Lys Glu Lys Leu Ala Glu
785 790 795 800

Leu Arg Lys Leu Cys Gln Gly Leu Phe Phe Arg Val Glu Glu Arg Lys
805 810 815

261/335

Lys Trp Pro Glu Arg Leu Ser Ala Leu Asp Asn Leu Leu Asn His Ser
820 825 830

Ser Met Phe Leu Lys Gly Ala Arg Leu Ile Pro Glu Met Asp Gln Ile
835 840 845

5 Phe Thr Glu Val Glu Met Thr Thr Leu Glu Lys Val Ile Asn Glu Thr
850 855 860

Trp Ala Trp Lys Asn Ala Thr Leu Ala Glu Gln Ala Lys Leu Pro Ala
865 870 875 880

Thr Glu Lys Pro Val Leu Leu Ser Lys Asp Ile Glu Ala Lys Met Met
10 885 890 895

Ala Leu Asp Arg Glu Val Gln Tyr Leu Leu Asn Lys Ala Lys Phe Thr
900 905 910

Lys Pro Arg Pro Arg Pro Lys Asp Lys Asn Gly Thr Arg Ala Glu Pro
915 920 925

15 Pro Leu Asn Ala Ser Ala Ser Asp Gln Gly Glu Lys Val Ile Pro Pro
930 935 940

Ala Gly Gln Thr Glu Asp Ala Glu Pro Ile Ser Glu Pro Glu Lys Val
945 950 955 960

Glu Thr Gly Ser Glu Pro Gly Asp Thr Glu Pro Leu Glu Leu Gly Gly
20 965 970 975

Pro Gly Ala Glu Pro Glu Gln Lys Glu Gln Ser Thr Gly Gln Lys Arg
980 985 990

Pro Leu Lys Asn Asp Glu Leu
995

<210> 86
<211> 271
5 <212> PRT
<213> Homo sapiens
<220>
<221> Peroxiredoxin 4
<222> (1)..(271)
10 <223> Accession No. as of 29 August 2003: Q13162
<400> 86

Met Glu Ala Leu Pro Leu Leu Ala Ala Thr Thr Pro Asp His Gly Arg
1 5 10 15
15 His Arg Arg Leu Leu Leu Leu Pro Leu Leu Leu Phe Leu Leu Pro Ala
20 25 30
Gly Ala Val Gln Gly Trp Glu Thr Glu Glu Arg Pro Arg Thr Arg Glu
35 40 45
Glu Glu Cys His Phe Tyr Ala Gly Gly Gln Val Tyr Pro Gly Glu Ala
20 50 55 60
Ser Arg Val Ser Val Ala Asp His Ser Leu His Leu Ser Lys Ala Lys
65 70 75 80
Ile Ser Lys Pro Ala Pro Tyr Trp Glu Gly Thr Ala Val Ile Asp Gly
85 90 95

263/335

Glu Phe Lys Glu Leu Lys Leu Thr Asp Tyr Arg Gly Lys Tyr Leu Val
100 105 110

Phe Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile
115 120 125

5 Ile Ala Phe Gly Asp Arg Leu Glu Glu Phe Arg Ser Ile Asn Thr Glu
130 135 140

Val Val Ala Cys Ser Val Asp Ser Gln Phe Thr His Leu Ala Trp Ile
145 150 155 160

Asn Thr Pro Arg Arg Gln Gly Gly Leu Gly Pro Ile Arg Ile Pro Leu
10 165 170 175

Leu Ser Asp Leu Thr His Gln Ile Ser Lys Asp Tyr Gly Val Tyr Leu
180 185 190

Glu Asp Ser Gly His Thr Leu Arg Gly Leu Phe Ile Ile Asp Asp Lys
195 200 205

15 Gly Ile Leu Arg Gln Ile Thr Leu Asn Asp Leu Pro Val Gly Arg Ser
210 215 220

Val Asp Glu Thr Leu Arg Leu Val Gln Ala Phe Gln Tyr Thr Asp Lys
225 230 235 240

His Gly Glu Val Cys Pro Ala Gly Trp Lys Pro Gly Ser Glu Thr Ile
20 245 250 255

Ile Pro Asp Pro Ala Gly Lys Leu Lys Tyr Phe Asp Lys Leu Asn
260 265 270

264/335

<210> 87

<211> 288

<212> PRT

<213> Homo sapiens

5 <220>

<221> MAWD binding protein

<222> (1)..(288)

<223> Accession No. as of 29 August 2003: P30039

<400> 87

10

Met Lys Leu Pro Ile Phe Ile Ala Asp Ala Phe Thr Ala Arg Ala Phe

1

5

10

15

Arg Gly Asn Pro Ala Ala Val Cys Leu Leu Glu Asn Glu Leu Asp Glu

20

25

30

15 Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser Glu Thr Ala

35

40

45

Phe Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln Ser Ser Cys

50

55

60

Phe Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val Pro Leu Cys Gly

20 65

70

75

80

His Ala Thr Leu Ala Ser Ala Ala Val Leu Phe His Lys Ile Lys Asn

85

90

95

Met Asn Ser Thr Leu Thr Phe Val Thr Leu Ser Gly Glu Leu Arg Ala

100

105

110

265/335

Arg Arg Ala Glu Asp Gly Ile Val Leu Asp Leu Pro Leu Tyr Pro Ala
115 120 125

His Pro Gln Asp Phe His Glu Val Glu Asp Leu Ile Lys Thr Ala Ile
130 135 140

5 Gly Asn Thr Leu Val Gln Asp Ile Cys Tyr Ser Pro Asp Thr Gln Lys
145 150 155 160

Leu Leu Val Arg Leu Ser Asp Val Tyr Asn Arg Ser Phe Leu Glu Asn
165 170 175

Leu Lys Val Asn Thr Glu Asn Leu Leu Gln Val Glu Asn Thr Gly Lys
10 180 185 190

Val Lys Gly Leu Ile Leu Thr Leu Lys Gly Glu Pro Gly Gly Gln Thr
195 200 205

Gln Ala Phe Asp Phe Tyr Ser Arg Tyr Phe Ala Pro Trp Val Gly Val
210 215 220

15 Ala Glu Asp Pro Val Thr Gly Ser Ala His Ala Val Leu Ser Ser Tyr
225 230 235 240

Trp Ser Gln His Leu Gly Lys Lys Glu Met His Ala Phe Gln Cys Ser
245 250 255

His Arg Gly Gly Glu Leu Gly Ile Ser Leu Arg Pro Asp Gly Arg Val
20 260 265 270

Asp Ile Arg Gly Gly Ala Ala Val Val Leu Glu Gly Thr Leu Thr Ala
275 280 285

266/335

<210> 88

<211> 511

<212> PRT

<213> Homo sapiens

5 <220>

<221> Alpha-amylase 2B precursor

<222> (1)..(511)

<223> Accession No. as of 29 August 2003: P19961

<400> 88

10

Met Lys Phe Phe Leu Leu Leu Phe Thr Ile Gly Phe Cys Trp Ala Gln

1 5 10 15

Tyr Ser Pro Asn Thr Gln Gln Gly Arg Thr Ser Ile Val His Leu Phe

20 25 30

15 Glu Trp Arg Trp Val Asp Ile Ala Leu Glu Cys Glu Arg Tyr Leu Ala

35 40 45

Pro Lys Gly Phe Gly Gly Val Gln Val Ser Pro Pro Asn Glu Asn Val

50 55 60

Ala Ile His Asn Pro Phe Arg Pro Trp Trp Glu Arg Tyr Gln Pro Val

20 65 70 75 80

Ser Tyr Lys Leu Cys Thr Arg Ser Gly Asn Glu Asp Glu Phe Arg Asn

85 90 95

Met Val Thr Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val Asp Ala

100 105 110

267/335

Val Ile Asn His Met Ser Gly Asn Ala Val Ser Ala Gly Thr Ser Ser
115 120 125

Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser Arg Asp Phe Pro Ala Val
130 135 140

5 Pro Tyr Ser Gly Trp Asp Phe Asn Asp Gly Lys Cys Lys Thr Gly Ser
145 150 155 160

Gly Asp Ile Glu Asn Tyr Asn Asp Ala Thr Gln Val Arg Asp Cys Arg
165 170 175

Leu Val Gly Leu Leu Asp Leu Ala Leu Glu Lys Asp Tyr Val Arg Ser
10 180 185 190

Lys Ile Ala Glu Tyr Met Asn His Leu Ile Asp Ile Gly Val Ala Gly
195 200 205

Phe Arg Leu Asp Ala Ser Lys His Met Trp Pro Gly Asp Ile Lys Ala
210 215 220

15 Ile Leu Asp Lys Leu His Asn Leu Asn Ser Asn Trp Phe Pro Ala Gly
225 230 235 240

Ser Lys Pro Phe Ile Tyr Gln Glu Val Ile Asp Leu Gly Gly Glu Pro
245 250 255

Ile Lys Ser Ser Asp Tyr Phe Gly Asn Gly Arg Val Thr Glu Phe Lys
20 260 265 270

Tyr Gly Ala Lys Leu Gly Thr Val Ile Arg Lys Trp Asn Gly Glu Lys
275 280 285

Met Ser Tyr Leu Lys Asn Trp Gly Glu Gly Trp Gly Phe Met Pro Ser
290 295 300

268/335

Asp Arg Ala Leu Val Phe Val Asp Asn His Asp Asn Gln Arg Gly His
305 310 315 320
Gly Ala Gly Gly Ala Ser Ile Leu Thr Phe Trp Asp Ala Arg Leu Tyr
325 330 335
5 Lys Met Ala Val Gly Phe Met Leu Ala His Pro Tyr Gly Phe Thr Arg
340 345 350
Val Met Ser Ser Tyr Arg Trp Pro Arg Gln Phe Gln Asn Gly Asn Asp
355 360 365
Val Asn Asp Trp Val Gly Pro Pro Asn Asn Asn Gly Val Ile Lys Glu
10 370 375 380
Val Thr Ile Asn Pro Asp Thr Thr Cys Gly Asn Asp Trp Val Cys Glu
385 390 395 400
His Arg Trp Arg Gln Ile Arg Asn Met Val Asn Phe Arg Asn Val Val
405 410 415
15 Asp Gly Gln Pro Phe Thr Asn Trp Tyr Asp Asn Gly Ser Asn Gln Val
420 425 430
Ala Phe Gly Arg Gly Asn Arg Gly Phe Ile Val Phe Asn Asn Asp Asp
435 440 445
Trp Thr Phe Ser Leu Thr Leu Gln Thr Gly Leu Pro Ala Gly Thr Tyr
20 450 455 460
Cys Asp Val Ile Ser Gly Asp Lys Ile Asn Gly Asn Cys Thr Gly Ile
465 470 475 480
Lys Ile Tyr Val Ser Asp Asp Gly Lys Ala His Phe Ser Ile Ser Asn
485 490 495

269/335

Ser Ala Glu Asp Pro Phe Ile Ala Ile His Ala Glu Ser Lys Leu

500

505

510

5 <210> 89

<211> 511

<212> PRT

<213> Homo sapiens

<220>

10 <221> Alpha-amylase, pancreatic precursor

<222> (1)..(511)

<223> Accession No. as of 29 August 2003: P04746

<400> 89

15 Met Lys Phe Phe Leu Leu Leu Phe Thr Ile Gly Phe Cys Trp Ala Gln

1

5

10

15

Tyr Ser Pro Asn Thr Gln Gln Gly Arg Thr Ser Ile Val His Leu Phe

20

25

30

Glu Trp Arg Trp Val Asp Ile Ala Leu Glu Cys Glu Arg Tyr Leu Ala

20

35

40

45

Pro Lys Gly Phe Gly Gly Val Gln Val Ser Pro Pro Asn Glu Asn Val

50

55

60

Ala Ile Tyr Asn Pro Phe Arg Pro Trp Trp Glu Arg Tyr Gln Pro Val

65

70

75

80

270/335

Ser Tyr Lys Leu Cys Thr Arg Ser Gly Asn Glu Asp Glu Phe Arg Asn
85 90 95

Met Val Thr Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val Asp Ala
100 105 110

5 Val Ile Asn His Met Cys Gly Asn Ala Val Ser Ala Gly Thr Ser Ser
115 120 125

Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser Arg Asp Phe Pro Ala Val
130 135 140

Pro Tyr Ser Gly Trp Asp Phe Asn Asp Gly Lys Cys Lys Thr Gly Ser
10 145 150 155 160

Gly Asp Ile Glu Asn Tyr Asn Asp Ala Thr Gln Val Arg Asp Cys Arg
165 170 175

Leu Thr Gly Leu Leu Asp Leu Ala Leu Glu Lys Asp Tyr Val Arg Ser
180 185 190

15 Lys Ile Ala Glu Tyr Met Asn His Leu Ile Asp Ile Gly Val Ala Gly
195 200 205

Phe Arg Leu Asp Ala Ser Lys His Met Trp Pro Gly Asp Ile Lys Ala
210 215 220

Ile Leu Asp Lys Leu His Asn Leu Asn Ser Asn Trp Phe Pro Ala Gly
20 225 230 235 240

Ser Lys Pro Phe Ile Tyr Gln Glu Val Ile Asp Leu Gly Gly Glu Pro
245 250 255

Ile Lys Ser Ser Asp Tyr Phe Gly Asn Gly Arg Val Thr Glu Phe Lys
260 265 270

271/335

Tyr Gly Ala Lys Leu Gly Thr Val Ile Arg Lys Trp Asn Gly Glu Lys
275 280 285

Met Ser Tyr Leu Lys Asn Trp Gly Glu Gly Trp Gly Phe Val Pro Ser
290 295 300

5 Asp Arg Ala Leu Val Phe Val Asp Asn His Asp Asn Gln Arg Gly His
305 310 315 320

Gly Ala Gly Gly Ala Ser Ile Leu Thr Phe Trp Asp Ala Arg Leu Tyr
325 330 335

Lys Met Ala Val Gly Phe Met Leu Ala His Pro Tyr Gly Phe Thr Arg
10 340 345 350

Val Met Ser Ser Tyr Arg Trp Pro Arg Gln Phe Gln Asn Gly Asn Asp
355 360 365

Val Asn Asp Trp Val Gly Pro Pro Asn Asn Asn Gly Val Ile Lys Glu
370 375 380

15 Val Thr Ile Asn Pro Asp Thr Thr Cys Gly Asn Asp Trp Val Cys Glu
385 390 395 400

His Arg Trp Arg Gln Ile Arg Asn Met Val Ile Phe Arg Asn Val Val
405 410 415

Asp Gly Gln Pro Phe Thr Asn Trp Tyr Asp Asn Gly Ser Asn Gln Val
20 420 425 430

Ala Phe Gly Arg Gly Asn Arg Gly Phe Ile Val Phe Asn Asn Asp Asp
435 440 445

Trp Ser Phe Ser Leu Thr Leu Gln Thr Gly Leu Pro Ala Gly Thr Tyr
450 455 460

272/335

Cys Asp Val Ile Ser Gly Asp Lys Ile Asn Gly Asn Cys Thr Gly Ile

465

470

475

480

Lys Ile Tyr Val Ser Asp Asp Gly Lys Ala His Phe Ser Ile Ser Asn

485

490

495

5 Ser Ala Glu Asp Pro Phe Ile Ala Ile His Ala Glu Ser Lys Leu

500

505

510

<210> 90

10 <211> 553

<212> PRT

<213> Homo sapiens

<220>

<221> ATP synthase alpha chain

15 <222> (1)..(553)

<223> Accession No. as of 29 August 2003: P25705

<400> 90

Met Leu Ser Val Arg Val Ala Ala Ala Val Val Arg Ala Leu Pro Arg

20 1

5

10

15

Arg Ala Gly Leu Val Ser Arg Asn Ala Leu Gly Ser Ser Phe Ile Ala

20

25

30

Ala Arg Asn Phe His Ala Ser Asn Thr His Leu Gln Lys Thr Gly Thr

35

40

45

273/335

Ala Glu Met Ser Ser Ile Leu Glu Glu Arg Ile Leu Gly Ala Asp Thr
50 55 60
Ser Val Asp Leu Glu Glu Thr Gly Arg Val Leu Ser Ile Gly Asp Gly
65 70 75 80
5 Ile Ala Arg Val His Gly Leu Arg Asn Val Gln Ala Glu Glu Met Val
85 90 95
Glu Phe Ser Ser Gly Leu Lys Gly Met Ser Leu Asn Leu Glu Pro Asp
100 105 110
Asn Val Gly Val Val Val Phe Gly Asn Asp Lys Leu Ile Lys Glu Gly
10 115 120 125
Asp Ile Val Lys Arg Thr Gly Ala Ile Val Asp Val Pro Val Gly Glu
130 135 140
Glu Leu Leu Gly Arg Val Val Asp Ala Leu Gly Asn Ala Ile Asp Gly
145 150 155 160
15 Lys Gly Pro Ile Gly Ser Lys Thr Arg Arg Arg Val Gly Leu Lys Ala
165 170 175
Pro Gly Ile Ile Pro Arg Ile Ser Val Arg Glu Pro Met Gln Thr Gly
180 185 190
Ile Lys Ala Val Asp Ser Leu Val Pro Ile Gly Arg Gly Gln Arg Glu
20 195 200 205
Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr Ser Ile Ala Ile Asp
210 215 220
Thr Ile Ile Asn Gln Lys Arg Phe Asn Asp Gly Ser Asp Glu Lys Lys
225 230 235 240

274/335

Lys Leu Tyr Cys Ile Tyr Val Ala Ile Gly Gln Lys Arg Ser Thr Val
245 250 255

Ala Gln Leu Val Lys Arg Leu Thr Asp Ala Asp Ala Met Lys Tyr Thr
260 265 270

5 Ile Val Val Ser Ala Thr Ala Ser Asp Ala Ala Pro Leu Gln Tyr Leu
275 280 285

Ala Pro Tyr Ser Gly Cys Ser Met Gly Glu Tyr Phe Arg Asp Asn Gly
290 295 300

Lys His Ala Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala
10 305 310 315 320

Tyr Arg Gln Met Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala
325 330 335

Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala
340 345 350

15 Ala Lys Met Asn Asp Ala Phe Gly Gly Gly Ser Leu Thr Ala Leu Pro
355 360 365

Val Ile Glu Thr Gln Ala Gly Asp Val Ser Ala Tyr Ile Pro Thr Asn
370 375 380

Val Ile Ser Ile Thr Asp Gly Gln Ile Phe Leu Glu Thr Glu Leu Phe
20 385 390 395 400

Tyr Lys Gly Ile Arg Pro Ala Ile Asn Val Gly Leu Ser Val Ser Arg
405 410 415

Val Gly Ser Ala Ala Gln Thr Arg Ala Met Lys Gln Val Ala Gly Thr
420 425 430

275/335

Met Lys Leu Glu Leu Ala Gln Tyr Arg Glu Val Ala Ala Phe Ala Gln

435

440

445

Phe Gly Ser Asp Leu Asp Ala Ala Thr Gln Gln Leu Leu Ser Arg Gly

450

455

460

5 Val Arg Leu Thr Glu Leu Leu Lys Gln Gly Gln Tyr Ser Pro Met Ala

465

470

475

480

Ile Glu Glu Gln Val Ala Val Ile Tyr Ala Gly Val Arg Gly Tyr Leu

485

490

495

Asp Lys Leu Glu Pro Ser Lys Ile Thr Lys Phe Glu Asn Ala Phe Leu

10

500

505

510

Ser His Val Val Ser Gln His Gln Ala Leu Leu Gly Thr Ile Arg Ala

515

520

525

Asp Gly Lys Ile Ser Glu Gln Ser Asp Ala Lys Leu Lys Glu Ile Val

530

535

540

15 Thr Asn Phe Leu Ala Gly Phe Glu Ala

545

550

<210> 91

20 <211> 742

<212> PRT

<213> Homo sapiens

<220>

<221> Bile-salt-activated lipase precursor

276/335

<222> (1)..(742)

<223> Accession No. as of 29 August 2003: P19835

<400> 91

5 Met Gly Arg Leu Gln Leu Val Val Leu Gly Leu Thr Cys Cys Trp Ala
1 5 10 15
Val Ala Ser Ala Ala Lys Leu Gly Ala Val Tyr Thr Glu Gly Gly Phe
20 25 30
Val Glu Gly Val Asn Lys Lys Leu Gly Leu Leu Gly Asp Ser Val Asp
10 35 40 45
Ile Phe Lys Gly Ile Pro Phe Ala Ala Pro Thr Lys Ala Leu Glu Asn
50 55 60
Pro Gln Pro His Pro Gly Trp Gln Gly Thr Leu Lys Ala Lys Asn Phe
65 70 75 80
15 Lys Lys Arg Cys Leu Gln Ala Thr Ile Thr Gln Asp Ser Thr Tyr Gly
85 90 95
Asp Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val Pro Gln Gly Arg Lys
100 105 110
Gln Val Ser Arg Asp Leu Pro Val Met Ile Trp Ile Tyr Gly Gly Ala
20 115 120 125
Phe Leu Met Gly Ser Gly His Gly Ala Asn Phe Leu Asn Asn Tyr Leu
130 135 140
Tyr Asp Gly Glu Glu Ile Ala Thr Arg Gly Asn Val Ile Val Val Thr
145 150 155 160

277/335

Phe Asn Tyr Arg Val Gly Pro Leu Gly Phe Leu Ser Thr Gly Asp Ala
165 170 175

Asn Leu Pro Gly Asn Tyr Gly Leu Arg Asp Gln His Met Ala Ile Ala
180 185 190

5 Trp Val Lys Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Asn Asn Ile
195 200 205

Thr Leu Phe Gly Glu Ser Ala Gly Gly Ala Ser Val Ser Leu Gln Thr
210 215 220

Leu Ser Pro Tyr Asn Lys Gly Leu Ile Arg Arg Ala Ile Ser Gln Ser
10 225 230 235 240

Gly Val Ala Leu Ser Pro Trp Val Ile Gln Lys Asn Pro Leu Phe Trp
245 250 255

Ala Lys Lys Val Ala Glu Lys Val Gly Cys Pro Val Gly Asp Ala Ala
260 265 270

15 Arg Met Ala Gln Cys Leu Lys Val Thr Asp Pro Arg Ala Leu Thr Leu
275 280 285

Ala Tyr Lys Val Pro Leu Ala Gly Leu Glu Tyr Pro Met Leu His Tyr
290 295 300

Val Gly Phe Val Pro Val Ile Asp Gly Asp Phe Ile Pro Ala Asp Pro
20 305 310 315 320

Ile Asn Leu Tyr Ala Asn Ala Ala Asp Ile Asp Tyr Ile Ala Gly Thr
325 330 335

Asn Asn Met Asp Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile
340 345 350

278/335

Asn Lys Gly Asn Lys Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val
355 360 365

Ser Glu Phe Thr Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe
370 375 380

5 Asp Val Tyr Thr Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys
385 390 395 400

Lys Lys Thr Val Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro
405 410 415

Thr Glu Ile Ala Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys
10 420 425 430

Thr Tyr Ala Tyr Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro
435 440 445

Lys Trp Val Gly Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly
450 455 460

15 Lys Pro Phe Ala Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val
465 470 475 480

Ser Lys Ala Met Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp
485 490 495

Pro Asn Met Gly Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr
20 500 505 510

Thr Glu Asn Ser Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser
515 520 525

Ser Met Lys Arg Ser Leu Arg Thr Asn Phe Leu Arg Tyr Trp Thr Leu
530 535 540

279/335

Thr Tyr Leu Ala Leu Pro Thr Val Thr Asp Gln Glu Ala Thr Pro Val
545 550 555 560
Pro Pro Thr Gly Asp Ser Glu Ala Thr Pro Val Pro Pro Thr Gly Asp
565 570 575
5 Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro
580 585 590
Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly
595 600 605
Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro
10 610 615 620
Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr
625 630 635 640
Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala
645 650 655
15 Pro Pro Val Pro Pro Thr Gly Asp Ala Gly Pro Pro Pro Val Pro Pro
660 665 670
Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly
675 680 685
Ala Pro Pro Val Thr Pro Thr Gly Asp Ser Glu Thr Ala Pro Val Pro
20 690 695 700
Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser
705 710 715 720
Glu Ala Ala Pro Val Pro Pro Thr Asp Asp Ser Lys Glu Ala Gln Met
725 730 735

Pro Ala Val Ile Arg Phe

740

5 <210> 92

<211> 467

<212> PRT

<213> Homo sapiens

<220>

10 <221> Pancreatic lipase related protein precursor

<222> (1)..(467)

<223> Accession No. as of 29 August 2003: P54315

<400> 92

15 Met Leu Ile Phe Trp Thr Ile Thr Leu Phe Leu Leu Gly Ala Ala Lys

1 5 10 15

Gly Lys Glu Val Cys Tyr Glu Asp Leu Gly Cys Phe Ser Asp Thr Glu

20 25 30

Pro Trp Gly Gly Thr Ala Ile Arg Pro Leu Lys Ile Leu Pro Trp Ser

20 35 40 45

Pro Glu Lys Ile Gly Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro

50 55 60

Asn Asn Phe Gln Ile Leu Leu Leu Ser Asp Pro Ser Thr Ile Glu Ala

65 70 75 80

281/335

Ser Asn Phe Gln Met Asp Arg Lys Thr Arg Phe Ile Ile His Gly Phe
85 90 95
Ile Asp Lys Gly Asp Glu Ser Trp Val Thr Asp Met Cys Lys Lys Leu
100 105 110
5 Phe Glu Val Glu Glu Val Asn Cys Ile Cys Val Asp Trp Lys Lys Gly
115 120 125
Ser Gln Ala Thr Tyr Thr Gln Ala Ala Asn Asn Val Arg Val Val Gly
130 135 140
Ala Gln Val Ala Gln Met Leu Asp Ile Leu Leu Thr Glu Tyr Ser Tyr
10 145 150 155 160
Pro Pro Ser Lys Val His Leu Ile Gly His Ser Leu Gly Ala His Val
165 170 175
Ala Gly Glu Ala Gly Ser Lys Thr Pro Gly Leu Ser Arg Ile Thr Gly
180 185 190
15 Leu Asp Pro Val Glu Ala Ser Phe Glu Ser Thr Pro Glu Glu Val Arg
195 200 205
Leu Asp Pro Ser Asp Ala Asp Phe Val Asp Val Ile His Thr Asp Ala
210 215 220
Ala Pro Leu Ile Pro Phe Leu Gly Phe Gly Thr Asn Gln Gln Met Gly
20 225 230 235 240
His Leu Asp Phe Phe Pro Asn Gly Gly Glu Ser Met Pro Gly Cys Lys
245 250 255
Lys Asn Ala Leu Ser Gln Ile Val Asp Leu Asp Gly Ile Trp Ala Gly
260 265 270

282/335

Thr Arg Asp Phe Val Ala Cys Asn His Leu Arg Ser Tyr Lys Tyr Tyr
275 280 285

Leu Glu Ser Ile Leu Asn Pro Asp Gly Phe Ala Ala Tyr Pro Cys Thr
290 295 300

5 Ser Tyr Lys Ser Phe Glu Ser Asp Lys Cys Phe Pro Cys Pro Asp Gln
305 310 315 320

Gly Cys Pro Gln Met Gly His Tyr Ala Asp Lys Phe Ala Gly Arg Thr
325 330 335

Ser Glu Glu Gln Gln Lys Phe Phe Leu Asn Thr Gly Glu Ala Ser Asn
10 340 345 350

Phe Ala Arg Trp Arg Tyr Gly Val Ser Ile Thr Leu Ser Gly Arg Thr
355 360 365

Ala Thr Gly Gln Ile Lys Val Ala Leu Phe Gly Asn Lys Gly Asn Thr
370 375 380

15 His Gln Tyr Ser Ile Phe Arg Gly Ile Leu Lys Pro Gly Ser Thr His
385 390 395 400

Ser Tyr Glu Phe Asp Ala Lys Leu Asp Val Gly Thr Ile Glu Lys Val
405 410 415

Lys Phe Leu Trp Asn Asn Asn Val Ile Asn Pro Thr Leu Pro Lys Val
20 420 425 430

Gly Ala Thr Lys Ile Thr Val Gln Lys Gly Glu Glu Lys Thr Val Tyr
435 440 445

Asn Phe Cys Ser Glu Asp Thr Val Arg Glu Asp Thr Leu Leu Thr Leu
450 455 460

Thr Pro Cys

465

5 <210> 93

<211> 469

<212> PRT

<213> Homo sapiens

<220>

10 <221> Pancreatic lipase related protein 2 precursor

<222> (1)..(469)

<223> Accession No. as of 29 August 2003: P54317

<400> 93

15 Met Leu Pro Pro Trp Thr Leu Gly Leu Leu Leu Leu Ala Thr Val Arg

1

5

10

15

Gly Lys Glu Val Cys Tyr Gly Gln Leu Gly Cys Phe Ser Asp Glu Lys

20

25

30

Pro Trp Ala Gly Thr Leu Gln Arg Pro Val Lys Leu Leu Pro Trp Ser

20

35

40

45

Pro Glu Asp Ile Asp Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro

50

55

60

Asn Asn Phe Gln Leu Ile Thr Gly Thr Glu Pro Asp Thr Ile Glu Ala

65

70

75

80

284/335

Ser Asn Phe Gln Leu Asp Arg Lys Thr Arg Phe Ile Ile His Gly Phe
85 90 95

Leu Asp Lys Ala Glu Asp Ser Trp Pro Ser Asp Met Cys Lys Lys Met
100 105 110

5 Phe Glu Val Glu Lys Val Asn Cys Ile Cys Val Asp Trp Arg His Gly
115 120 125

Ser Arg Ala Met Tyr Thr Gln Ala Val Gln Asn Ile Arg Val Val Gly
130 135 140

Ala Glu Thr Ala Phe Leu Ile Gln Ala Leu Ser Thr Gln Leu Gly Tyr
10 145 150 155 160

Ser Leu Glu Asp Val His Val Ile Gly His Ser Leu Gly Ala His Thr
165 170 175

Ala Ala Glu Ala Gly Arg Arg Leu Gly Gly Arg Val Gly Arg Ile Thr
180 185 190

15 Gly Leu Asp Pro Ala Gly Pro Cys Phe Gln Asp Glu Pro Glu Glu Val
195 200 205

Arg Leu Asp Pro Ser Asp Ala Val Phe Val Asp Val Ile His Thr Asp
210 215 220

Ser Ser Pro Ile Val Pro Ser Leu Gly Phe Gly Met Ser Gln Lys Val
20 225 230 235 240

Gly His Leu Asp Phe Phe Pro Asn Gly Gly Lys Glu Met Pro Gly Cys
245 250 255

Lys Lys Asn Val Leu Ser Thr Ile Thr Asp Ile Asp Gly Ile Trp Glu
260 265 270

285/335

Gly Ile Gly Gly Phe Val Ser Cys Asn His Leu Arg Ser Phe Glu Tyr
275 280 285

Tyr Ser Ser Ser Val Leu Asn Pro Asp Gly Phe Leu Gly Tyr Pro Cys
290 295 300

5 Ala Ser Tyr Asp Glu Phe Gln Glu Ser Lys Cys Phe Pro Cys Pro Ala
305 310 315 320

Glu Gly Cys Pro Lys Met Gly His Tyr Ala Asp Gln Phe Lys Gly Lys
325 330 335

Thr Ser Ala Val Glu Gln Thr Phe Phe Leu Asn Thr Gly Glu Ser Gly
10 340 345 350

Asn Phe Thr Ser Trp Arg Tyr Lys Val Ser Val Thr Leu Ser Gly Lys
355 360 365

Glu Lys Val Asn Gly Tyr Ile Arg Ile Ala Leu Tyr Gly Ser Asn Glu
370 375 380

15 Asn Ser Lys Gln Tyr Glu Ile Phe Lys Gly Ser Leu Lys Pro Asp Ala
385 390 395 400

Ser His Thr Cys Ala Ile Asp Val Asp Phe Asn Val Gly Lys Ile Gln
405 410 415

Lys Val Lys Phe Leu Trp Asn Lys Arg Gly Ile Asn Leu Ser Glu Pro
20 420 425 430

Lys Leu Gly Ala Ser Gln Ile Thr Val Gln Ser Gly Glu Asp Gly Thr
435 440 445

Glu Tyr Asn Phe Cys Ser Ser Asp Thr Val Glu Glu Asn Val Leu Gln
450 455 460

Ser Leu Tyr Pro Cys

465

5 <210> 94

<211> 465

<212> PRT

<213> Homo sapiens

<220>

10 <221> Triacylglycerol lipase, pancreatic precursor

<222> (1)..(465)

<223> Accession No. as of 29 August 2003: P16233

<400> 94

15 Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Leu Gly Ala Val Ala Gly

1 5 10 15

Lys Glu Val Cys Tyr Glu Arg Leu Gly Cys Phe Ser Asp Asp Ser Pro

20 25 30

Trp Ser Gly Ile Thr Glu Arg Pro Leu His Ile Leu Pro Trp Ser Pro

20 35 40 45

Lys Asp Val Asn Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro Asn

50 55 60

Asn Phe Gln Glu Val Ala Ala Asp Ser Ser Ser Ile Ser Gly Ser Asn

65 70 75 80

287/335

Phe Lys Thr Asn Arg Lys Thr Arg Phe Ile Ile His Gly Phe Ile Asp
85 90 95

Lys Gly Glu Glu Asn Trp Leu Ala Asn Val Cys Lys Asn Leu Phe Lys
100 105 110

5 Val Glu Ser Val Asn Cys Ile Cys Val Asp Trp Lys Gly Gly Ser Arg
115 120 125

Thr Gly Tyr Thr Gln Ala Ser Gln Asn Ile Arg Ile Val Gly Ala Glu
130 135 140

Val Ala Tyr Phe Val Glu Phe Leu Gln Ser Ala Phe Gly Tyr Ser Pro
10 145 150 155 160

Ser Asn Val His Val Ile Gly His Ser Leu Gly Ala His Ala Ala Gly
165 170 175

Glu Ala Gly Arg Arg Thr Asn Gly Thr Ile Gly Arg Ile Thr Gly Leu
180 185 190

15 Asp Pro Ala Glu Pro Cys Phe Gln Gly Thr Pro Glu Leu Val Arg Leu
195 200 205

Asp Pro Ser Asp Ala Lys Phe Val Asp Val Ile His Thr Asp Gly Ala
210 215 220

Pro Ile Val Pro Asn Leu Gly Phe Gly Met Ser Gln Val Val Gly His
20 225 230 235 240

Leu Asp Phe Phe Pro Asn Gly Gly Val Glu Met Pro Gly Cys Lys Lys
245 250 255

Asn Ile Leu Ser Gln Ile Val Asp Ile Asp Gly Ile Trp Glu Gly Thr
260 265 270

288/335

Arg Asp Phe Ala Ala Cys Asn His Leu Arg Ser Tyr Lys Tyr Tyr Thr
275 280 285

Asp Ser Ile Val Asn Pro Asp Gly Phe Ala Gly Phe Pro Cys Ala Ser
290 295 300

5 Tyr Asn Val Phe Thr Ala Asn Lys Cys Phe Pro Cys Pro Ser Gly Gly
305 310 315 320

Cys Pro Gln Met Gly His Tyr Ala Asp Arg Tyr Pro Gly Lys Thr Asn
325 330 335

Asp Val Gly Gln Lys Phe Tyr Leu Asp Thr Gly Asp Ala Ser Asn Phe
10 340 345 350

Ala Arg Trp Arg Tyr Lys Val Ser Val Thr Leu Ser Gly Lys Lys Val
355 360 365

Thr Gly His Ile Leu Val Ser Leu Phe Gly Asn Lys Gly Asn Ser Lys
370 375 380

15 Gln Tyr Glu Ile Phe Lys Gly Thr Leu Lys Pro Asp Ser Thr His Ser
385 390 395 400

Asn Glu Phe Asp Ser Asp Val Asp Val Gly Asp Leu Gln Met Val Lys
405 410 415

Phe Ile Trp Tyr Asn Asn Val Ile Asn Pro Thr Leu Pro Arg Val Gly
20 420 425 430

Ala Ser Lys Ile Ile Val Glu Thr Asn Val Gly Lys Gln Phe Asn Phe
435 440 445

Cys Ser Pro Glu Thr Val Arg Glu Glu Val Leu Leu Thr Leu Thr Pro
450 455 460

Cys

465

5 <210> 95

<211> 572

<212> PRT

<213> Homo sapiens

<220>

10 <221> Dihydropyrimidinase related protein-2

<222> (1)..(572)

<223> Accession No. as of 29 August 2003: Q16555

<400> 95

15 Met Ser Tyr Gln Gly Lys Lys Asn Ile Pro Arg Ile Thr Ser Asp Arg

1 5 10 15

Leu Leu Ile Lys Gly Gly Lys Ile Val Asn Asp Asp Gln Ser Phe Tyr

20 25 30

Ala Asp Ile Tyr Met Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn

20 35 40 45

Leu Ile Val Pro Gly Gly Val Lys Thr Ile Glu Ala His Ser Arg Met

50 55 60

Val Ile Pro Gly Gly Ile Asp Val His Thr Arg Phe Gln Met Pro Asp

65 70 75 80

290/335

Gln Gly Met Thr Ser Ala Asp Asp Phe Phe Gln Gly Thr Lys Ala Ala
85 90 95

Leu Ala Gly Gly Thr Thr Met Ile Ile Asp His Val Val Pro Glu Pro
100 105 110

5 Gly Thr Ser Leu Leu Ala Ala Phe Asp Gln Trp Arg Glu Trp Ala Asp
115 120 125

Ser Lys Ser Cys Cys Asp Tyr Ser Leu His Val Asp Ile Ser Glu Trp
130 135 140

His Lys Gly Ile Gln Glu Glu Met Glu Ala Leu Val Lys Asp His Gly
10 145 150 155 160

Val Asn Ser Phe Leu Val Tyr Met Ala Phe Lys Asp Arg Phe Gln Leu
165 170 175

Thr Asp Cys Gln Ile Tyr Glu Val Leu Ser Val Ile Arg Asp Ile Gly
180 185 190

15 Ala Ile Ala Gln Val His Ala Glu Asn Gly Asp Ile Ile Ala Glu Glu
195 200 205

Gln Gln Arg Ile Leu Asp Leu Gly Ile Thr Gly Pro Glu Gly His Val
210 215 220

Leu Ser Arg Pro Glu Glu Val Glu Ala Glu Ala Val Asn Arg Ala Ile
20 225 230 235 240

Thr Ile Ala Asn Gln Thr Asn Cys Pro Leu Tyr Ile Thr Lys Val Met
245 250 255

Ser Lys Ser Ser Ala Glu Val Ile Ala Gln Ala Arg Lys Lys Gly Thr
260 265 270

291/335

Val Val Tyr Gly Glu Pro Ile Thr Ala Ser Leu Gly Thr Asp Gly Ser
275 280 285

His Tyr Trp Ser Lys Asn Trp Ala Lys Ala Ala Phe Val Thr Ser
290 295 300

5 Pro Pro Leu Ser Pro Asp Pro Thr Thr Pro Asp Phe Leu Asn Ser Leu
305 310 315 320

Leu Ser Cys Gly Asp Leu Gln Val Thr Gly Ser Ala His Cys Thr Phe
325 330 335

Asn Thr Ala Gln Lys Ala Val Gly Lys Asp Asn Phe Thr Leu Ile Pro
10 340 345 350

Glu Gly Thr Asn Gly Thr Glu Glu Arg Met Ser Val Ile Trp Asp Lys
355 360 365

Ala Val Val Thr Gly Lys Met Asp Glu Asn Gln Phe Val Ala Val Thr
370 375 380

15 Ser Thr Asn Ala Ala Lys Val Phe Asn Leu Tyr Pro Arg Lys Gly Arg
385 390 395 400

Ile Ala Val Gly Ser Asp Ala Asp Leu Val Ile Trp Asp Pro Asp Ser
405 410 415

Val Lys Thr Ile Ser Ala Lys Thr His Asn Ser Ser Leu Glu Tyr Asn
20 420 425 430

Ile Phe Glu Gly Met Glu Cys Arg Gly Ser Pro Leu Val Val Ile Ser
435 440 445

Gln Gly Lys Ile Val Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly
450 455 460

292/335

Ser Gly Arg Tyr Ile Pro Arg Lys Pro Phe Pro Asp Phe Val Tyr Lys
465 470 475 480
Arg Ile Lys Ala Arg Ser Arg Leu Ala Glu Leu Arg Gly Val Pro Arg
485 490 495
5 Gly Leu Tyr Asp Gly Pro Val Cys Glu Val Ser Val Thr Pro Lys Thr
500 505 510
Val Thr Pro Ala Ser Ser Ala Lys Thr Ser Pro Ala Lys Gln Gln Ala
515 520 525
Pro Pro Val Arg Asn Leu His Gln Ser Gly Phe Ser Leu Ser Gly Ala
10 530 535 540
Gln Ile Asp Asp Asn Ile Pro Arg Arg Thr Thr Gln Arg Ile Val Ala
545 550 555 560
Pro Pro Gly Gly Arg Ala Asn Ile Thr Ser Leu Gly
565 570

15

<210> 96

<211> 500

<212> PRT

20 <213> Homo sapiens

<220>

<221> 4-aminobutyrate aminotransferase, mitochondrial precursor

<222> (1)..(500)

<223> Accession No. as of 29 August 2003: P80404

293/335

<400> 96

Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1 5 10 15
5 Thr Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala
20 25 30
Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr
35 40 45
Glu Val Pro Gly Pro Arg Ser Gln Glu Leu Met Lys Gln Leu Asn Ile
10 50 55 60
Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr Glu Glu Ser
65 70 75 80
Arg Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu
85 90 95
15 Tyr Ser Gln Ile Ser Ser Val Pro Ile Gly Tyr Ser Asp Pro Ala Leu
100 105 110
Val Lys Leu Ile Gln Gln Pro Gln Asn Ala Ser Met Phe Val Asn Arg
115 120 125
Pro Ala Leu Glu Ile Leu Pro Pro Glu Asn Phe Val Glu Lys Leu Arg
20 130 135 140
Gln Ser Leu Leu Ser Val Ala Pro Lys Gly Met Ser Gln Leu Ile Thr
145 150 155 160
Met Ala Cys Gly Ser Cys Ser Asn Glu Asn Ala Leu Lys Thr Ile Phe
165 170 175

294/335

Met Trp Tyr Arg Ser Lys Glu Arg Gly Gln Arg Gly Phe Ser Lys Glu
180 185 190
Glu Leu Glu Thr Cys Met Ile Asn Gln Ala Pro Trp Cys Pro Asp Tyr
195 200 205
5 Ser Ile Leu Ser Phe Met Gly Ser Phe His Gly Arg Thr Met Gly Cys
210 215 220
Leu Ala Thr Thr His Ser Lys Ala Ile His Lys Ile Asp Ile Pro Ser
225 230 235 240
Phe Asp Trp Pro Ile Ala Pro Phe Pro Arg Leu Lys Tyr Pro Leu Glu
10 245 250 255
Glu Phe Val Lys Glu Asn Gln Gln Glu Glu Ala Gly Cys Leu Glu Glu
260 265 270
Val Glu Asp Leu Ile Val Lys Tyr Arg Lys Lys Lys Lys Thr Val Ala
275 280 285
15 Gly Ile Ile Val Glu Pro Ile Gln Ser Glu Gly Gly Asp Asn His Ala
290 295 300
Ser Asp Asp Phe Phe Arg Lys Leu Arg Asp Ile Ala Arg Lys His Cys
305 310 315 320
Cys Ala Phe Leu Val Asp Glu Val Gln Thr Gly Gly Gly Cys Thr Gly
20 325 330 335
Lys Phe Trp Ala His Glu His Trp Gly Leu Asp Asp Pro Ala Asp Val
340 345 350
Met Thr Phe Ser Lys Lys Met Met Thr Gly Gly Phe Phe Leu Lys Glu
355 360 365

295/335

Glu Phe Arg Pro Asn Ala Pro Tyr Arg Ile Phe Asn Thr Trp Leu Gly
370 375 380
Asp Pro Ser Lys Asn Leu Leu Leu Ala Glu Val Ile Asn Ile Ile Lys
385 390 395 400
5 Arg Glu Asp Leu Leu Asn Asn Ala Ala His Ala Gly Lys Ala Leu Leu
405 410 415
Thr Gly Leu Leu Asp Leu Gln Ala Arg Tyr Pro Gln Phe Ile Ser Arg
420 425 430
Val Arg Gly Arg Gly Thr Phe Cys Ser Phe Asp Thr Pro Asp Asp Ser
10 435 440 445
Ile Arg Asn Lys Leu Ile Leu Ile Ala Arg Asn Lys Gly Val Val Leu
450 455 460
Gly Gly Cys Gly Asp Lys Ser Ile Arg Phe Arg Pro Thr Leu Val Phe
465 470 475 480
15 Arg Asp His His Ala His Leu Phe Leu Asn Ile Phe Ser Asp Ile Leu
485 490 495
Ala Asp Phe Lys
500

20

<210> 97

<211> 423

<212> PRT

<213> Homo sapiens

<220>

<221> Glycine amidiontransferase, mitochondrial precursor

<222> (1)..(423)

<223> Accession No. as of 29 August 2003: P50440

5 <400> 97

Met Leu Arg Val Arg Cys Leu Arg Gly Gly Ser Arg Gly Ala Glu Ala
1 5 10 15
Val His Tyr Ile Gly Ser Arg Leu Gly Arg Thr Leu Thr Gly Trp Val
10 20 25 30
Gln Arg Thr Phe Gln Ser Thr Gln Ala Ala Thr Ala Ser Ser Arg Asn
35 40 45
Ser Cys Ala Ala Asp Asp Lys Ala Thr Glu Pro Leu Pro Lys Asp Cys
50 55 60
15 Pro Val Ser Ser Tyr Asn Glu Trp Asp Pro Leu Glu Glu Val Ile Val
65 70 75 80
Gly Arg Ala Glu Asn Ala Cys Val Pro Pro Phe Thr Ile Glu Val Lys
85 90 95
Ala Asn Thr Tyr Glu Lys Tyr Trp Pro Phe Tyr Gln Lys Gln Gly Gly
20 100 105 110
His Tyr Phe Pro Lys Asp His Leu Lys Lys Ala Val Ala Glu Ile Glu
115 120 125
Glu Met Cys Asn Ile Leu Lys Thr Glu Gly Val Thr Val Arg Arg Pro
130 135 140

297/335

Asp Pro Ile Asp Trp Ser Leu Lys Tyr Lys Thr Pro Asp Phe Glu Ser
145 150 155 160
Thr Gly Leu Tyr Ser Ala Met Pro Arg Asp Ile Leu Ile Val Val Gly
165 170 175
5 Asn Glu Ile Ile Glu Ala Pro Met Ala Trp Arg Ser Arg Phe Phe Glu
180 185 190
Tyr Arg Ala Tyr Arg Ser Ile Ile Lys Asp Tyr Phe His Arg Gly Ala
195 200 205
Lys Trp Thr Thr Ala Pro Lys Pro Thr Met Ala Asp Glu Leu Tyr Asn
10 210 215 220
Gln Asp Tyr Pro Ile His Ser Val Glu Asp Arg His Lys Leu Ala Ala
225 230 235 240
Gln Gly Lys Phe Val Thr Thr Glu Phe Glu Pro Cys Phe Asp Ala Ala
245 250 255
15 Asp Phe Ile Arg Ala Gly Arg Asp Ile Phe Ala Gln Arg Ser Gln Val
260 265 270
Thr Asn Tyr Leu Gly Ile Glu Trp Met Arg Arg His Leu Ala Pro Asp
275 280 285
Tyr Arg Val His Ile Ile Ser Phe Lys Asp Pro Asn Pro Met His Ile
20 290 295 300
Asp Ala Thr Phe Asn Ile Ile Gly Pro Gly Ile Val Leu Ser Asn Pro
305 310 315 320
Asp Arg Pro Cys His Gln Ile Asp Leu Phe Lys Lys Ala Gly Trp Thr
325 330 335

298/335

Ile Ile Thr Pro Pro Thr Pro Ile Ile Pro Asp Asp His Pro Leu Trp
340 345 350
Met Ser Ser Lys Trp Leu Ser Met Asn Val Leu Met Leu Asp Glu Lys
355 360 365
5 Arg Val Met Val Asp Ala Asn Glu Val Pro Ile Gln Lys Met Phe Glu
370 375 380
Lys Leu Gly Ile Thr Thr Ile Lys Val Asn Ile Arg Asn Ala Asn Ser
385 390 395 400
Leu Gly Gly Gly Phe His Cys Trp Thr Cys Asp Val Arg Arg Arg Gly
10 405 410 415
Thr Leu Gln Ser Tyr Leu Asp
420

15 <210> 98

<211> 654

<212> PRT

<213> Homo sapiens

<220>

20 <221> GRP 78

<222> (1)..(654)

<223> Accession No. as of 29 August 2003: P11021

<220>

<221> misc_feature

- <222> (302)..(302)
- <223> Xaa can be any naturally occurring amino acid
- <220>
- <221> misc_feature
- 5 <222> (329)..(329)
- <223> Xaa can be any naturally occurring amino acid
- <220>
- <221> misc_feature
- <222> (344)..(344)
- 10 <223> Xaa can be any naturally occurring amino acid
- <220>
- <221> misc_feature
- <222> (461)..(461)
- <223> Xaa can be any naturally occurring amino acid
- 15 <400> 98

Met Lys Leu Ser Leu Val Ala Ala Met Leu Leu Leu Leu Ser Ala

1 5 10 15

Ala Arg Ala Lys Glu Glu Asp Met Gly Thr Val Val Ala Ile His Leu

20 20 25 30

Gly Thr Thr Tyr Pro Cys Val Gly Val Phe Lys Asn Gly Arg Met Glu

35 40 45

Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Met Pro Ser Tyr Val Ala

50 55 60

300/335

Phe Thr Pro Glu Gly Glu Cys Leu Ile Gly Asp Ala Ala Lys Asn Gln
65 70 75 80
Leu Thr Ser Asn Pro Lys Asn Thr Val Phe Asp Ala Lys Arg Leu Ile
85 90 95
5 Gly Arg Arg Trp His Asp Pro Ser Val Gln Gln Asp Ile Glu Phe Leu
100 105 110
Pro Phe Lys Val Val Glu Lys Asn Thr Lys Ser Tyr Ile Gln Ile Asp
115 120 125
Val Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Lys Glu Ile Ser Ala
10 130 135 140
Met Val Leu Thr Lys Met Lys Glu Asn Ala Glu Ala Tyr Leu Gly Lys
145 150 155 160
Val Thr His Ala Val Val Thr Ala Pro Ala Tyr Phe Asn Asp Ala Gln
165 170 175
15 Cys Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Asp Leu Asn Val Met
180 185 190
Arg Ile Ile Asn Lys Pro Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp
195 200 205
Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly Gly Gly
20 210 215 220
Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe Lys Val
225 230 235 240
Val Ala Thr Asn Gly Asp Thr Tyr Leu Gly Gly Glu Asp Phe Asp Gln
245 250 255

301/335

Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr Gly Lys
260 265 270

Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Trp Arg Lys Val
275 280 285

5 Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Xaa Val Ile
290 295 300

Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu Thr
305 310 315 320

Gln Ala Lys Phe Glu Glu Leu Asn Xaa Asp Leu Phe Gln Ser Thr Met
10 325 330 335

Lys Pro Ser Gln Arg Ser Val Xaa Lys Val Leu Glu Asp Ser Asp Leu
340 345 350

Lys Lys Ser Asp Ile Asp Glu Thr Val Leu Val Gly Gly Phe Thr Gln
355 360 365

15 Ile Pro Lys Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu
370 375 380

Leu Ser Arg Gly Ile Ser Pro Tyr Glu Ala Val Ala Tyr Gly Ala Ala
385 390 395 400

Val Gln Ala Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val
20 405 410 415

Leu Leu Asp Ile Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly
420 425 430

Val Met Thr Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys
435 440 445

Ser Gln Ile Phe Ser Thr Ala Phe Asp Asn Gln Pro Xaa Thr Ile Lys
450 455 460

Val Tyr Glu Gly Lys Gln Pro Leu Thr Lys Asp Asn His Leu Leu Gly
465 470 475 480

5 Thr Phe Asp Leu Thr Gly Ile Pro Pro Ala Pro Cys Gly Val Pro Gln
485 490 495

Ile Glu Val Thr Phe Glu Met Asp Val Ser Asp Ile Leu Gln Val Thr
500 505 510

Ala Lys Asp Lys Gly Thr Arg Tyr Lys Asn Lys Ile Thr Ile Thr Asn
10 515 520 525

Asp Gln Asn His Leu Thr Pro Glu Asp Ile Glu Arg Met Val Asn Asp
530 535 540

Ala Glu Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Cys Thr Asp
545 550 555 560

15 Thr Arg Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile
565 570 575

Gly Asp Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu
580 585 590

Thr Met Glu Lys Thr Val Glu Glu Lys Thr Glu Trp Leu Glu Ser His
20 595 600 605

Gln Asp Ala Asp Thr Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu
610 615 620

Glu Ile Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro
625 630 635 640

303/335

Pro Pro Thr Gly Glu Glu Asp Thr Ala Glu Lys Asp Glu Leu

645

650

5 <210> 99

<211> 325

<212> PRT

<213> Homo sapiens

<220>

10 <221> Eukaryotic translation initiation factor 3 subunit 2

<222> (1)..(325)

<223> Accession No. as of 29 August 2003: Q13347

<400> 99

15 Met Lys Pro Ile Leu Leu Gln Gly His Glu Arg Ser Ile Thr Gln Ile

1 5 10 15

Lys Tyr Asn Arg Glu Gly Asp Leu Leu Phe Thr Val Ala Lys Asp Pro

20 25 30

Ile Val Asn Val Trp Tyr Ser Val Asn Gly Glu Arg Leu Gly Thr Tyr

20 35 40 45

Met Gly His Thr Gly Ala Val Trp Cys Val Asp Ala Asp Trp Asp Thr

50 55 60

Lys His Val Leu Thr Gly Ser Ala Asp Asn Ser Cys Arg Leu Trp Asp

65 70 75 80

304/335

Cys Glu Thr Gly Lys Gln Leu Ala Leu Leu Lys Thr Asn Ser Ala Val
85 90 95

Arg Thr Cys Gly Phe Asp Phe Gly Gly Asn Ile Ile Met Phe Ser Thr
100 105 110

5 Asp Lys Gln Met Gly Tyr Gln Cys Phe Val Ser Phe Phe Asp Leu Arg
115 120 125

Asp Pro Ser Gln Ile Asp Asn Asn Glu Pro Tyr Met Lys Ile Pro Cys
130 135 140

Asn Asp Ser Lys Ile Thr Ser Ala Val Trp Gly Pro Leu Gly Glu Cys
10 145 150 155 160

Ile Ile Ala Gly His Glu Ser Gly Glu Leu Asn Gln Tyr Ser Ala Lys
165 170 175

Ser Gly Glu Val Leu Val Asn Val Lys Glu His Ser Arg Gln Ile Asn
180 185 190

15 Asp Ile Gln Leu Ser Arg Asp Met Thr Met Phe Val Thr Ala Ser Lys
195 200 205

Asp Asn Thr Ala Lys Leu Phe Asp Ser Thr Thr Leu Glu His Gln Lys
210 215 220

Thr Phe Arg Thr Glu Arg Pro Val Asn Ser Ala Ala Leu Ser Pro Asn
20 225 230 235 240

Tyr Asp His Val Val Leu Gly Gly Gly Gln Glu Ala Met Asp Val Thr
245 250 255

Thr Thr Ser Thr Arg Ile Gly Lys Phe Glu Ala Arg Phe Phe His Leu
260 265 270

305/335

Ala Phe Glu Glu Glu Phe Gly Arg Val Lys Gly His Phe Gly Pro Ile

275

280

285

Asn Ser Val Ala Phe His Pro Asp Gly Lys Ser Tyr Ser Ser Gly Gly

290

295

300

5 Glu Asp Gly Tyr Val Arg Ile His Tyr Phe Asp Pro Gln Tyr Phe Glu

305

310

315

320

Phe Glu Phe Glu Ala

325

10

<210> 100

<211> 572

<212> PRT

<213> Homo sapiens

15 <220>

<221> Dihydropyrimidinase related protein-2

<222> (1)..(572)

<223> Accession No. as of 29 August 2003: Q16555

<400> 100

20

Met Ser Tyr Gln Gly Lys Lys Asn Ile Pro Arg Ile Thr Ser Asp Arg

1

5

10

15

Leu Leu Ile Lys Gly Gly Lys Ile Val Asn Asp Asp Gln Ser Phe Tyr

20

25

30

306/335

Ala Asp Ile Tyr Met Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn
35 40 45

Leu Ile Val Pro Gly Gly Val Lys Thr Ile Glu Ala His Ser Arg Met
50 55 60

5 Val Ile Pro Gly Gly Ile Asp Val His Thr Arg Phe Gln Met Pro Asp
65 70 75 80

Gln Gly Met Thr Ser Ala Asp Asp Phe Phe Gln Gly Thr Lys Ala Ala
85 90 95

Leu Ala Gly Gly Thr Thr Met Ile Ile Asp His Val Val Pro Glu Pro
10 100 105 110

Gly Thr Ser Leu Leu Ala Ala Phe Asp Gln Trp Arg Glu Trp Ala Asp
115 120 125

Ser Lys Ser Cys Cys Asp Tyr Ser Leu His Val Asp Ile Ser Glu Trp
130 135 140

15 His Lys Gly Ile Gln Glu Glu Met Glu Ala Leu Val Lys Asp His Gly
145 150 155 160

Val Asn Ser Phe Leu Val Tyr Met Ala Phe Lys Asp Arg Phe Gln Leu
165 170 175

Thr Asp Cys Gln Ile Tyr Glu Val Leu Ser Val Ile Arg Asp Ile Gly
20 180 185 190

Ala Ile Ala Gln Val His Ala Glu Asn Gly Asp Ile Ile Ala Glu Glu
195 200 205

Gln Gln Arg Ile Leu Asp Leu Gly Ile Thr Gly Pro Glu Gly His Val
210 215 220

307/335

Leu Ser Arg Pro Glu Glu Val Glu Ala Glu Ala Val Asn Arg Ala Ile
225 230 235 240
Thr Ile Ala Asn Gln Thr Asn Cys Pro Leu Tyr Ile Thr Lys Val Met
245 250 255
5 Ser Lys Ser Ser Ala Glu Val Ile Ala Gln Ala Arg Lys Lys Gly Thr
260 265 270
Val Val Tyr Gly Glu Pro Ile Thr Ala Ser Leu Gly Thr Asp Gly Ser
275 280 285
His Tyr Trp Ser Lys Asn Trp Ala Lys Ala Ala Ala Phe Val Thr Ser
10 290 295 300
Pro Pro Leu Ser Pro Asp Pro Thr Thr Pro Asp Phe Leu Asn Ser Leu
305 310 315 320
Leu Ser Cys Gly Asp Leu Gln Val Thr Gly Ser Ala His Cys Thr Phe
325 330 335
15 Asn Thr Ala Gln Lys Ala Val Gly Lys Asp Asn Phe Thr Leu Ile Pro
340 345 350
Glu Gly Thr Asn Gly Thr Glu Glu Arg Met Ser Val Ile Trp Asp Lys
355 360 365
Ala Val Val Thr Gly Lys Met Asp Glu Asn Gln Phe Val Ala Val Thr
20 370 375 380
Ser Thr Asn Ala Ala Lys Val Phe Asn Leu Tyr Pro Arg Lys Gly Arg
385 390 395 400
Ile Ala Val Gly Ser Asp Ala Asp Leu Val Ile Trp Asp Pro Asp Ser
405 410 415

308/335

Val Lys Thr Ile Ser Ala Lys Thr His Asn Ser Ser Leu Glu Tyr Asn
420 425 430
Ile Phe Glu Gly Met Glu Cys Arg Gly Ser Pro Leu Val Val Ile Ser
435 440 445
5 Gln Gly Lys Ile Val Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly
450 455 460
Ser Gly Arg Tyr Ile Pro Arg Lys Pro Phe Pro Asp Phe Val Tyr Lys
465 470 475 480
Arg Ile Lys Ala Arg Ser Arg Leu Ala Glu Leu Arg Gly Val Pro Arg
10 485 490 495
Gly Leu Tyr Asp Gly Pro Val Cys Glu Val Ser Val Thr Pro Lys Thr
500 505 510
Val Thr Pro Ala Ser Ser Ala Lys Thr Ser Pro Ala Lys Gln Gln Ala
515 520 525
15 Pro Pro Val Arg Asn Leu His Gln Ser Gly Phe Ser Leu Ser Gly Ala
530 535 540
Gln Ile Asp Asp Asn Ile Pro Arg Arg Thr Thr Gln Arg Ile Val Ala
545 550 555 560
Pro Pro Gly Gly Arg Ala Asn Ile Thr Ser Leu Gly
20 565 570

<210> 101

<211> 561

<212> PRT

<213> Homo sapiens

<220>

<221> Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM)

5 <222> (1)..(561)

<223> Accession No. as of 29 August 2003: P36871

<400> 101

Val Lys Ile Val Thr Val Lys Thr Gln Ala Tyr Gln Asp Gln Lys Pro
10 1 5 10 15
Gly Thr Ser Gly Leu Arg Lys Arg Val Lys Val Phe Gln Ser Ser Ala
20 25 30
Asn Tyr Ala Glu Asn Phe Ile Gln Ser Ile Ile Ser Thr Val Glu Pro
35 40 45
15 Ala Gln Arg Gln Glu Ala Thr Leu Val Val Gly Gly Asp Gly Arg Phe
50 55 60
Tyr Met Lys Glu Ala Ile Gln Leu Ile Ala Arg Ile Ala Ala Ala Asn
65 70 75 80
Gly Ile Gly Arg Leu Val Ile Gly Gln Asn Gly Ile Leu Ser Thr Pro
20 85 90 95
Ala Val Ser Cys Ile Ile Arg Lys Ile Lys Ala Ile Gly Gly Ile Ile
100 105 110
Leu Thr Ala Ser His Asn Pro Gly Gly Pro Asn Gly Asp Phe Gly Ile
115 120 125

310/335

Lys Phe Asn Ile Ser Asn Gly Gly Pro Ala Pro Glu Ala Ile Thr Asp
130 135 140

Lys Ile Phe Gln Ile Ser Lys Thr Ile Glu Glu Tyr Ala Val Cys Pro
145 150 155 160

5 Asp Leu Lys Val Asp Leu Gly Val Leu Gly Lys Gln Gln Phe Asp Leu
165 170 175

Glu Asn Lys Phe Lys Pro Phe Thr Val Glu Ile Val Asp Ser Val Glu
180 185 190

Ala Tyr Ala Thr Met Leu Arg Ser Ile Phe Asp Phe Ser Ala Leu Lys
10 195 200 205

Glu Leu Leu Ser Gly Pro Asn Arg Leu Lys Ile Arg Ile Asp Ala Met
210 215 220

His Gly Val Val Gly Pro Tyr Val Lys Lys Ile Leu Cys Glu Glu Leu
225 230 235 240

15 Gly Ala Pro Ala Asn Ser Ala Val Asn Cys Val Pro Leu Glu Asp Phe
245 250 255

Gly Gly His His Pro Asp Pro Asn Leu Thr Tyr Ala Ala Asp Leu Val
260 265 270

Glu Thr Met Lys Ser Gly Glu His Asp Phe Gly Ala Ala Phe Asp Gly
20 275 280 285

Asp Gly Asp Arg Asn Met Ile Leu Gly Lys His Gly Phe Phe Val Asn
290 295 300

Pro Ser Asp Ser Val Ala Val Ile Ala Ala Asn Ile Phe Ser Ile Pro
305 310 315 320

311/335

Tyr Phe Gln Gln Thr Gly Val Arg Gly Phe Ala Arg Ser Met Pro Thr
325 330 335

Ser Gly Ala Leu Asp Arg Val Ala Ser Ala Thr Lys Ile Ala Leu Tyr
340 345 350

5 Glu Thr Pro Thr Gly Trp Lys Phe Phe Gly Asn Leu Met Asp Ala Ser
355 360 365

Lys Leu Ser Leu Cys Gly Glu Glu Ser Phe Gly Thr Gly Ser Asp His
370 375 380

Ile Arg Glu Lys Asp Gly Leu Trp Ala Val Leu Ala Trp Leu Ser Ile
10 385 390 395 400

Leu Ala Thr Arg Lys Gln Ser Val Glu Asp Ile Leu Lys Asp His Trp
405 410 415

Gln Lys Tyr Gly Arg Asn Phe Phe Thr Arg Tyr Asp Tyr Glu Glu Val
420 425 430

15 Glu Ala Glu Gly Ala Asn Lys Met Met Lys Asp Leu Glu Ala Leu Met
435 440 445

Phe Asp Arg Ser Phe Val Gly Lys Gln Phe Ser Ala Asn Asp Lys Val
450 455 460

Tyr Thr Val Glu Lys Ala Asp Asn Phe Glu Tyr Ser Asp Pro Val Asp
20 465 470 475 480

Gly Ser Ile Ser Arg Asn Gln Gly Leu Arg Leu Ile Phe Thr Asp Gly
485 490 495

Ser Arg Ile Val Phe Arg Leu Ser Gly Thr Gly Ser Ala Gly Ala Thr
500 505 510

312/335

Ile Arg Leu Tyr Ile Asp Ser Tyr Glu Lys Asp Val Ala Lys Ile Asn

515

520

525

Gln Asp Pro Gln Val Met Leu Ala Pro Leu Ile Ser Ile Ala Leu Lys

530

535

540

5 Val Ser Gln Leu Gln Glu Arg Thr Gly Arg Thr Ala Pro Thr Val Ile

545

550

555

560

Thr

10

<210> 102

<211> 263

<212> PRT

<213> Homo sapiens

15 <220>

<221> Proteasome subunit alpha type 1

<222> (1)..(263)

<223> Accession No. as of 29 August 2003: P25786

<400> 102

20

Met Phe Arg Asn Gln Tyr Asp Asn Asp Val Thr Val Trp Ser Pro Gln

1

5

10

15

Gly Arg Ile His Gln Ile Glu Tyr Ala Met Glu Ala Val Lys Gln Gly

20

25

30

313/335

Ser Ala Thr Val Gly Leu Lys Ser Lys Thr His Ala Val Leu Val Ala
35 40 45

Leu Lys Arg Ala Gln Ser Glu Leu Ala Ala His Gln Lys Lys Ile Leu
50 55 60

5 His Val Asp Asn His Ile Gly Ile Ser Ile Ala Gly Leu Thr Ala Asp
65 70 75 80

Ala Arg Leu Leu Cys Asn Phe Met Arg Gln Glu Cys Leu Asp Ser Arg
85 90 95

Phe Val Phe Asp Arg Pro Leu Pro Val Ser Arg Leu Val Ser Leu Ile
10 100 105 110

Gly Ser Lys Thr Gln Ile Pro Thr Gln Arg Tyr Gly Arg Arg Pro Tyr
115 120 125

Gly Val Gly Leu Leu Ile Ala Gly Tyr Asp Asp Met Gly Pro His Ile
130 135 140

15 Phe Gln Thr Cys Pro Ser Ala Asn Tyr Phe Asp Cys Arg Ala Met Ser
145 150 155 160

Ile Gly Ala Arg Ser Gln Ser Ala Arg Thr Tyr Leu Glu Arg His Met
165 170 175

Ser Glu Phe Met Glu Cys Asn Leu Asn Glu Leu Val Lys His Gly Leu
20 180 185 190

Arg Ala Leu Arg Glu Thr Leu Pro Ala Glu Gln Asp Leu Thr Thr Lys
195 200 205

Asn Val Ser Ile Gly Ile Val Gly Lys Asp Leu Glu Phe Thr Ile Tyr
210 215 220

314/335

Asp Asp Asp Asp Val Ser Pro Phe Leu Glu Gly Leu Glu Glu Arg Pro

225 230 235 240

Gln Arg Lys Ala Gln Pro Ala Gln Pro Ala Asp Glu Pro Ala Glu Lys

245 250 255

5 Ala Asp Glu Pro Met Glu His

260

<210> 103

10 <211> 205

<212> PRT

<213> Homo sapiens

<220>

<221> Heat shock 27 kDa protein

15 <222> (1)..(205)

<223> Accession No. as of 29 August 2003: P04792

<400> 103

Met Thr Glu Arg Arg Val Pro Phe Ser Leu Leu Arg Gly Pro Ser Trp

20 1 5 10 15

Asp Pro Phe Arg Asp Trp Tyr Pro His Ser Arg Leu Phe Asp Gln Ala

20 25 30

Phe Gly Leu Pro Arg Leu Pro Glu Glu Trp Ser Gln Trp Leu Gly Gly

35 40 45

315/335

Ser Ser Trp Pro Gly Tyr Val Arg Pro Leu Pro Pro Ala Ala Ile Glu
50 55 60

Ser Pro Ala Val Ala Ala Pro Ala Tyr Ser Arg Ala Leu Ser Arg Gln
65 70 75 80

5 Leu Ser Ser Gly Val Ser Glu Ile Arg His Thr Ala Asp Arg Trp Arg
85 90 95

Val Ser Leu Asp Val Asn His Phe Ala Pro Asp Glu Leu Thr Val Lys
100 105 110

Thr Lys Asp Gly Val Val Glu Ile Thr Gly Lys His Glu Glu Arg Gln
10 115 120 125

Asp Glu His Gly Tyr Ile Ser Arg Cys Phe Thr Arg Lys Tyr Thr Leu
130 135 140

Pro Pro Gly Val Asp Pro Thr Gln Val Ser Ser Ser Leu Ser Pro Glu
145 150 155 160

15 Gly Thr Leu Thr Val Glu Ala Pro Met Pro Lys Leu Ala Thr Gln Ser
165 170 175

Asn Glu Ile Thr Ile Pro Val Thr Phe Glu Ser Arg Ala Gln Leu Gly
180 185 190

Gly Pro Glu Ala Ala Lys Ser Asp Glu Thr Ala Ala Lys
20 195 200 205

<210> 104

<211> 868

316/335

<212> PRT

<213> Homo sapiens

<220>

<221> Programmed cell death 6 interacting protein (Hp95)

5 <222> (1)..(868)

<223> Accession No. as of 29 August 2003: Q8WUM4

<400> 104

Met Ala Thr Phe Ile Ser Val Gln Leu Lys Lys Thr Ser Glu Val Asp
10 1 5 10 15
Leu Ala Lys Pro Leu Val Lys Phe Ile Gln Gln Thr Tyr Pro Ser Gly
20 25 30
Gly Glu Glu Gln Ala Gln Tyr Cys Arg Ala Ala Glu Glu Leu Ser Lys
35 40 45
15 Leu Arg Arg Ala Ala Val Gly Arg Pro Leu Asp Lys His Glu Gly Ala
50 55 60
Leu Glu Thr Leu Leu Arg Tyr Tyr Asp Gln Ile Cys Ser Ile Glu Pro
65 70 75 80
Lys Phe Pro Phe Ser Glu Asn Gln Ile Cys Leu Thr Phe Thr Trp Lys
20 85 90 95
Asp Ala Phe Asp Lys Gly Ser Leu Phe Gly Gly Ser Val Lys Leu Ala
100 105 110
Leu Ala Ser Leu Gly Tyr Glu Lys Ser Cys Val Leu Phe Asn Cys Ala
115 120 125

317/335

Ala Leu Ala Ser Gln Ile Ala Ala Glu Gln Asn Leu Asp Asn Asp Glu
130 135 140

Gly Leu Lys Ile Ala Ala Lys His Tyr Gln Phe Ala Ser Gly Ala Phe
145 150 155 160

5 Leu His Ile Lys Glu Thr Val Leu Ser Ala Leu Ser Arg Glu Pro Thr
165 170 175

Val Asp Ile Ser Pro Asp Thr Val Gly Thr Leu Ser Leu Ile Met Leu
180 185 190

Ala Gln Ala Gln Glu Val Phe Phe Leu Lys Ala Thr Arg Asp Lys Met
10 195 200 205

Lys Asp Ala Ile Ile Ala Lys Leu Ala Asn Gln Ala Ala Asp Tyr Phe
210 215 220

Gly Asp Ala Phe Lys Gln Cys Gln Tyr Lys Asp Thr Leu Pro Lys Glu
225 230 235 240

15 Val Phe Pro Val Leu Ala Ala Lys His Cys Ile Met Gln Ala Asn Ala
245 250 255

Glu Tyr His Gln Ser Ile Leu Ala Lys Gln Gln Lys Lys Phe Gly Glu
260 265 270

Glu Ile Ala Arg Leu Gln His Ala Ala Glu Leu Ile Lys Thr Val Ala
20 275 280 285

Ser Arg Tyr Asp Glu Tyr Val Asn Val Lys Asp Phe Ser Asp Lys Ile
290 295 300

Asn Arg Ala Leu Ala Ala Ala Lys Lys Asp Asn Asp Phe Ile Tyr His
305 310 315 320

318/335

Asp Arg Val Pro Asp Leu Lys Asp Leu Asp Pro Ile Gly Lys Ala Thr
325 330 335

Leu Val Lys Ser Thr Pro Val Asn Val Pro Ile Ser Gln Lys Phe Thr
340 345 350

5 Asp Leu Phe Glu Lys Met Val Pro Val Ser Val Gln Gln Ser Leu Ala
355 360 365

Ala Tyr Asn Gln Arg Lys Ala Asp Leu Val Asn Arg Ser Ile Ala Gln
370 375 380

Met Arg Glu Ala Thr Thr Leu Ala Asn Gly Val Leu Ala Ser Leu Asn
10 385 390 395 400

Leu Pro Ala Ala Ile Glu Asp Val Ser Gly Asp Thr Val Pro Gln Ser
405 410 415

Ile Leu Thr Lys Ser Arg Ser Val Ile Glu Gln Gly Gly Ile Gln Thr
420 425 430

15 Val Asp Gln Leu Ile Lys Glu Leu Pro Glu Leu Leu Gln Arg Asn Arg
435 440 445

Glu Ile Leu Asp Glu Ser Leu Arg Leu Leu Asp Glu Glu Glu Ala Thr
450 455 460

Asp Asn Asp Leu Arg Ala Lys Phe Lys Glu Arg Trp Gln Arg Thr Pro
20 465 470 475 480

Ser Asn Glu Leu Tyr Lys Pro Leu Arg Ala Glu Gly Thr Asn Phe Arg
485 490 495

Thr Val Leu Asp Lys Ala Val Gln Ala Asp Gly Gln Val Lys Glu Cys
500 505 510

319/335

Tyr Gln Ser His Arg Asp Thr Ile Val Leu Leu Cys Lys Pro Glu Pro
515 520 525

Glu Leu Asn Ala Ala Ile Pro Ser Ala Asn Pro Ala Lys Thr Met Gln
530 535 540

5 Gly Ser Glu Val Val Asn Val Leu Lys Ser Leu Leu Ser Asn Leu Asp
545 550 555 560

Glu Val Lys Lys Glu Arg Glu Gly Leu Glu Asn Asp Leu Lys Ser Val
565 570 575

Asn Phe Asp Met Thr Ser Lys Phe Leu Thr Ala Leu Ala Gln Asp Gly
10 580 585 590

Val Ile Asn Glu Glu Ala Leu Ser Val Thr Glu Leu Asp Arg Val Tyr
595 600 605

Gly Gly Leu Thr Thr Lys Val Gln Glu Ser Leu Lys Lys Gln Glu Gly
610 615 620

15 Leu Leu Lys Asn Ile Gln Val Ser His Gln Glu Phe Ser Lys Met Lys
625 630 635 640

Gln Ser Asn Asn Glu Ala Asn Leu Arg Glu Glu Val Leu Lys Asn Leu
645 650 655

Ala Thr Ala Tyr Asp Asn Phe Val Glu Leu Val Ala Asn Leu Lys Glu
20 660 665 670

Gly Thr Lys Phe Tyr Asn Glu Leu Thr Glu Ile Leu Val Arg Phe Gln
675 680 685

Asn Lys Cys Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu
690 695 700

320/335

Leu Leu Lys Asp Leu Gln Gln Ser Ile Ala Arg Glu Pro Ser Ala Pro
705 710 715 720
Ser Ile Pro Thr Pro Ala Tyr Gln Ser Ser Pro Ala Gly Gly His Ala
725 730 735
5 Pro Thr Pro Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro
740 745 750
Gln Pro Pro Ala Arg Pro Pro Pro Pro Val Leu Pro Ala Asn Arg Ala
755 760 765
Pro Ser Ala Thr Ala Pro Ser Pro Val Gly Ala Gly Thr Ala Ala Pro
10 770 775 780
Ala Pro Ser Gln Thr Pro Gly Ser Ala Pro Pro Pro Gln Ala Gln Gly
785 790 795 800
Pro Pro Tyr Pro Thr Tyr Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro
805 810 815
15 Met Pro Met Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro
820 825 830
Tyr Pro Pro Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly
835 840 845
Pro Gln Gln Pro Ser Tyr Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr
20 850 855 860
Tyr Pro Gln Gln
865

321/335

<210> 105

<211> 280

<212> PRT

<213> Homo sapiens

5 <220>

<221> Similar to four and a half LIM domains 3

<222> (1)..(280)

<223> Accession No. as of 29 August 2003: Q9BVA2.

<400> 105

10

Met Ser Glu Ser Phe Asp Cys Ala Lys Cys Asn Glu Ser Leu Tyr Gly

1 5 10 15

Arg Lys Tyr Ile Gln Thr Asp Ser Gly Pro Tyr Cys Val Pro Cys Tyr

20 25 30

15 Asp Asn Thr Phe Ala Asn Thr Cys Ala Glu Cys Gln Gln Leu Ile Gly

35 40 45

His Asp Ser Arg Glu Leu Phe Tyr Glu Asp Arg His Phe His Glu Gly

50 55 60

Cys Phe Arg Cys Cys Arg Cys Gln Arg Ser Leu Ala Asp Glu Pro Phe

20 65 70 75 80

Thr Cys Gln Asp Ser Glu Leu Leu Cys Asn Asp Cys Tyr Cys Ser Ala

85 90 95

Phe Ser Ser Gln Cys Ser Ala Cys Gly Glu Thr Val Met Pro Gly Ser

100 105 110

322/335

Arg Lys Leu Glu Tyr Gly Gly Gln Thr Trp His Glu His Cys Phe Leu
115 120 125

Cys Ser Gly Cys Glu Gln Pro Leu Gly Ser Arg Ser Phe Val Pro Asp
130 135 140

5 Lys Gly Ala His Tyr Cys Val Pro Cys Tyr Glu Asn Lys Phe Ala Pro
145 150 155 160

Arg Cys Ala Arg Cys Ser Lys Thr Leu Thr Gln Gly Gly Val Thr Tyr
165 170 175

Arg Asp Gln Pro Trp His Arg Glu Cys Leu Val Cys Thr Gly Cys Gln
10 180 185 190

Thr Pro Leu Ala Gly Gln Gln Phe Thr Ser Arg Asp Glu Asp Pro Tyr
195 200 205

Cys Val Ala Cys Phe Gly Glu Leu Phe Ala Pro Lys Cys Ser Ser Cys
210 215 220

15 Lys Arg Pro Ile Val Gly Leu Gly Gly Gly Lys Tyr Val Ser Phe Glu
225 230 235 240

Asp Arg His Trp His His Asn Cys Phe Ser Cys Ala Arg Cys Ser Thr
245 250 255

Ser Leu Val Gly Gln Gly Phe Val Pro Asp Gly Asp Gln Val Leu Cys
20 260 265 270

Gln Gly Cys Ser Gln Ala Gly Pro
275 280

<210> 106

<211> 280

<212> PRT

<213> Homo sapiens

5 <220>

<221> Skeletal muscle LIM-protein 2 (SLIM 2)

<222> (1)..(280)

<223> Accession No. as of 29 August 2003: Q13643

<400> 106

10

Met Ser Glu Ser Phe Asp Cys Ala Lys Cys Asn Glu Ser Leu Tyr Gly

1 5 10 15

Arg Lys Tyr Ile Gln Thr Asp Ser Gly Pro Tyr Cys Val Pro Cys Tyr

20 25 30

15 Asp Asn Thr Phe Ala Asn Thr Cys Ala Glu Cys Gln Gln Leu Ile Gly

35 40 45

His Asp Ser Arg Glu Leu Phe Tyr Glu Asp Arg His Phe His Glu Gly

50 55 60

Cys Phe Arg Cys Cys Arg Cys Gln Arg Ser Leu Ala Asp Glu Pro Phe

20 65 70 75 80

Thr Arg Gln Asp Ser Glu Leu Leu Cys Asn Asp Cys Tyr Cys Ser Ala

85 90 95

Phe Ser Ser Gln Cys Ser Ala Cys Gly Glu Thr Val Met Pro Gly Ser

100 105 110

Arg Lys Leu Glu Tyr Gly Gly Gln Thr Trp His Glu His Cys Phe Leu
115 120 125

Cys Ile Gly Cys Glu Gln Pro Leu Gly Ser Arg Pro Phe Val Pro Asp
130 135 140

5 Lys Gly Ala His Tyr Cys Val Pro Cys Tyr Glu Asn Asn Phe Ala Pro
145 150 155 160

Arg Cys Ala Arg Cys Thr Lys Thr Leu Thr Gln Gly Gly Leu Thr Tyr
165 170 175

Arg Asp Leu Pro Trp His Pro Lys Cys Leu Val Cys Thr Gly Cys Gln
10 180 185 190

Thr Pro Leu Ala Gly Gln Gln Phe Thr Ser Arg Asp Glu Asp Pro Tyr
195 200 205

Cys Val Ala Cys Phe Gly Glu Leu Phe Ala Pro Lys Cys Ser Ser Cys
210 215 220

15 Lys Arg Pro Ile Val Gly Leu Gly Gly Gly Lys Tyr Val Ser Phe Glu
225 230 235 240

Asp Arg His Trp His His Asn Cys Phe Thr Cys Asp Arg Cys Ser Asn
245 250 255

Ser Leu Val Gly Gln Gly Phe Val Pro Asp Gly Asp Gln Val Leu Cys
20 260 265 270

Gln Gly Cys Ser Gln Ala Gly Pro
275 280

325/335

<210> 107

<211> 133

<212> PRT

<213> Homo sapiens

5 <220>

<221> Cytochrome b5

<222> (1)..(133)

<223> Accession No. as of 29 August 2003: P00167

<400> 107

10

Ala Glu Gln Ser Asp Glu Ala Val Lys Tyr Tyr Thr Leu Glu Glu Ile

1 5 10 15

Gln Lys His Asn His Ser Lys Ser Thr Trp Leu Ile Leu His His Lys

20 25 30

15 Val Tyr Asp Leu Thr Lys Phe Leu Glu Glu His Pro Gly Gly Glu Glu

35 40 45

Val Leu Arg Glu Gln Ala Gly Gly Asp Ala Thr Glu Asn Phe Glu Asp

50 55 60

Val Gly His Ser Thr Asp Ala Arg Glu Met Ser Lys Thr Phe Ile Ile

20 65 70 75 80

Gly Glu Leu His Pro Asp Asp Arg Pro Lys Leu Asn Lys Pro Pro Glu

85 90 95

Thr Leu Ile Thr Thr Ile Asp Ser Ser Ser Ser Trp Trp Thr Asn Trp

100 105 110

326/335

Val Ile Pro Ala Ile Ser Ala Val Ala Val Ala Leu Met Tyr Arg Leu

115

120

125

Tyr Met Ala Glu Asp

130

5

<210> 108

<211> 175

<212> PRT

10 <213> Homo sapiens

<220>

<221> Pancreatitis-associated protein 1 precursor

<222> (1)..(175)

<223> Accession No. as of 29 August 2003: Q06141

15 <400> 108

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu Ser

1

5

10

15

Cys Leu Met Leu Leu Ser Gln Val Gln Gly Glu Glu Pro Gln Arg Glu

20

20

25

30

Leu Pro Ser Ala Arg Ile Arg Cys Pro Lys Gly Ser Lys Ala Tyr Gly

35

40

45

Ser His Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser Trp Thr Asp Ala

50

55

60

327/335

Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Asn	Leu	Val	Ser	Val	Leu	
65							70						75		80	
Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	Leu	Val	Lys	Ser	Ile	Gly	
							85						90		95	
5	Asn	Ser	Tyr	Ser	Tyr	Val	Trp	Ile	Gly	Leu	His	Asp	Pro	Thr	Gln	Gly
							100						105		110	
Thr	Glu	Pro	Asn	Gly	Glu	Gly	Trp	Glu	Trp	Ser	Ser	Ser	Asp	Val	Met	
							115						120		125	
Asn	Tyr	Phe	Ala	Trp	Glu	Arg	Asn	Pro	Ser	Thr	Ile	Ser	Ser	Pro	Gly	
10																
	130						135						140			
His	Cys	Ala	Ser	Leu	Ser	Arg	Ser	Thr	Ala	Phe	Leu	Arg	Trp	Lys	Asp	
145							150						155		160	
Tyr	Asn	Cys	Asn	Val	Arg	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Thr	Asp		
							165						170		175	

15

<210> 109

<211> 1028

<212> PRT

20 <213> Homo sapiens

<220>

<221> Collagen alpha 1(VI) chain precursor

<222> (1) .. (1028)

<223> Accession No. as of 29 August 2003: P12109

<400> 109

Met Arg Ala Ala Arg Ala Leu Leu Pro Leu Leu Leu Gln Ala Cys Trp
1 5 10 15
5 Thr Ala Ala Gln Asp Glu Pro Glu Thr Pro Arg Ala Val Ala Phe Gln
20 25 30
Asp Cys Pro Val Asp Leu Phe Phe Val Leu Asp Thr Ser Glu Ser Val
35 40 45
Ala Leu Arg Leu Lys Pro Tyr Gly Ala Leu Val Asp Lys Val Lys Ser
10 50 55 60
Phe Thr Lys Arg Phe Ile Asp Asn Leu Arg Asp Arg Tyr Tyr Arg Cys
65 70 75 80
Asp Arg Asn Leu Val Trp Asn Ala Gly Ala Leu His Tyr Ser Asp Glu
85 90 95
15 Val Glu Ile Ile Gln Gly Leu Thr Arg Met Pro Gly Gly Arg Asp Ala
100 105 110
Leu Lys Ser Ser Val Asp Ala Val Lys Tyr Phe Gly Lys Gly Thr Tyr
115 120 125
Thr Asp Cys Ala Ile Lys Lys Gly Leu Glu Gln Leu Leu Val Gly Gly
20 130 135 140
Ser His Leu Lys Glu Asn Lys Tyr Leu Ile Val Val Thr Asp Gly His
145 150 155 160
Pro Leu Glu Gly Tyr Lys Glu Pro Cys Gly Gly Leu Glu Asp Ala Val
165 170 175

329/335

Asn Glu Ala Lys His Leu Gly Val Lys Val Phe Ser Val Ala Ile Thr
180 185 190
Pro Asp His Leu Glu Pro Arg Leu Ser Ile Ile Ala Thr Asp His Thr
195 200 205
5 Tyr Arg Arg Asn Phe Thr Ala Ala Asp Trp Gly Gln Ser Arg Asp Ala
210 215 220
Glu Glu Ala Ile Ser Gln Thr Ile Asp Thr Ile Val Asp Met Ile Lys
225 230 235 240
Asn Asn Val Glu Gln Val Cys Cys Ser Phe Glu Cys Gln Pro Ala Arg
10 245 250 255
Gly Pro Pro Gly Leu Arg Gly Asp Pro Gly Phe Glu Gly Glu Arg Gly
260 265 270
Lys Pro Gly Leu Pro Gly Glu Lys Gly Glu Ala Gly Asp Pro Gly Arg
275 280 285
15 Pro Gly Asp Leu Gly Pro Val Gly Tyr Gln Gly Met Lys Gly Glu Lys
290 295 300
Gly Ser Arg Gly Glu Lys Gly Ser Arg Gly Pro Lys Gly Tyr Lys Gly
305 310 315 320
Glu Lys Gly Lys Arg Gly Ile Asp Gly Val Asp Gly Val Lys Gly Glu
20 325 330 335
Met Gly Tyr Pro Gly Leu Pro Gly Cys Lys Gly Ser Pro Gly Phe Asp
340 345 350
Gly Ile Gln Gly Pro Pro Gly Pro Lys Gly Asp Pro Gly Ala Phe Gly
355 360 365

330/335

Leu Lys Gly Glu Lys Gly Glu Pro Gly Ala Asp Gly Glu Ala Gly Arg
370 375 380

Pro Gly Ala Arg Gly Pro Ser Gly Asp Glu Gly Pro Ala Gly Glu Pro
385 390 395 400

5 Gly Pro Pro Gly Glu Lys Gly Glu Ala Gly Asp Glu Gly Asn Pro Gly
405 410 415

Pro Asp Gly Ala Pro Gly Glu Arg Gly Gly Pro Gly Glu Arg Gly Pro
420 425 430

Arg Gly Thr Pro Gly Pro Arg Gly Pro Arg Gly Asp Pro Gly Glu Ala
10 435 440 445

Gly Pro Gln Gly Asp Gln Gly Arg Glu Gly Pro Val Gly Val Pro Gly
450 455 460

Asp Pro Gly Glu Ala Gly Pro Ile Gly Pro Lys Gly Tyr Arg Gly Asp
465 470 475 480

15 Glu Gly Pro Pro Gly Ser Glu Gly Ala Arg Gly Ala Pro Gly Pro Ala
485 490 495

Gly Pro Pro Gly Asp Pro Gly Leu Met Gly Glu Arg Gly Glu Asp Gly
500 505 510

Pro Ala Gly Asn Gly Thr Glu Gly Phe Pro Gly Phe Pro Gly Tyr Pro
20 515 520 525

Gly Asn Arg Gly Ala Pro Gly Ile Asn Gly Thr Lys Gly Tyr Pro Gly
530 535 540

Leu Lys Gly Asp Glu Gly Glu Ala Gly Asp Pro Gly Asp Asp Asn Asn
545 550 555 560

331/335

Asp Ile Ala Pro Arg Gly Val Lys Gly Ala Lys Gly Tyr Arg Gly Pro
565 570 575

Glu Gly Pro Gln Gly Pro Pro Gly His Gln Gly Pro Pro Gly Pro Asp
580 585 590

5 Glu Cys Glu Ile Leu Asp Ile Ile Met Lys Met Cys Ser Cys Cys Glu
595 600 605

Cys Lys Cys Gly Pro Ile Asp Leu Leu Phe Val Leu Asp Ser Ser Glu
610 615 620

Ser Ile Gly Leu Gln Asn Phe Glu Ile Ala Lys Asp Phe Val Val Lys
10 625 630 635 640

Val Ile Asp Arg Leu Ser Arg Asp Glu Leu Val Lys Phe Glu Pro Gly
645 650 655

Gln Ser Tyr Ala Gly Val Val Gln Tyr Ser His Ser Gln Met Gln Glu
660 665 670

15 His Val Ser Leu Arg Ser Pro Ser Ile Arg Asn Val Gln Glu Leu Lys
675 680 685

Glu Ala Ile Lys Ser Leu Gln Trp Met Ala Gly Gly Thr Phe Thr Gly
690 695 700

Glu Ala Leu Gln Tyr Thr Arg Asp Gln Leu Leu Pro Pro Ser Pro Asn
20 705 710 715 720

Asn Arg Ile Ala Leu Val Ile Thr Asp Gly Arg Ser Asp Thr Gln Arg
725 730 735

Asp Thr Thr Pro Leu Asn Val Leu Cys Ser Pro Gly Ile Gln Val Val
740 745 750

332/335

Ser Val Gly Ile Lys Asp Val Phe Asp Phe Ile Pro Gly Ser Asp Gln
755 760 765

Leu Asn Val Ile Ser Cys Gln Gly Leu Ala Pro Ser Gln Gly Arg Pro
770 775 780

5 Gly Leu Ser Leu Val Lys Glu Asn Tyr Ala Glu Leu Leu Glu Asp Ala
785 790 795 800

Phe Leu Lys Asn Val Thr Ala Gln Ile Cys Ile Asp Lys Lys Cys Pro
805 810 815

Asp Tyr Thr Cys Pro Ile Thr Phe Ser Ser Pro Ala Asp Ile Thr Ile
10 820 825 830

Leu Leu Asp Gly Ser Ala Ser Val Gly Ser His Asn Phe Asp Thr Thr
835 840 845

Lys Arg Phe Ala Lys Arg Leu Ala Glu Arg Phe Leu Thr Ala Gly Arg
850 855 860

15 Thr Asp Pro Ala His Asp Val Arg Val Ala Val Val Gln Tyr Ser Gly
865 870 875 880

Thr Gly Gln Gln Arg Pro Glu Arg Ala Ser Leu Gln Phe Leu Gln Asn
885 890 895

Tyr Thr Ala Leu Ala Ser Ala Val Asp Ala Met Asp Phe Ile Asn Asp
20 900 905 910

Ala Thr Asp Val Asn Asp Ala Leu Gly Tyr Val Thr Arg Phe Tyr Arg
915 920 925

Glu Ala Ser Ser Gly Ala Ala Lys Lys Arg Leu Leu Leu Phe Ser Asp
930 935 940

333/335

Gly Asn Ser Gln Gly Ala Thr Pro Ala Ala Ile Glu Lys Ala Val Gln

945

950

955

960

Glu Ala Gln Arg Ala Gly Ile Glu Ile Phe Val Val Val Val Gly Arg

965

970

975

5 Gln Val Asn Glu Pro His Ile Arg Val Leu Val Thr Gly Lys Thr Ala

980

985

990

Glu Tyr Asp Val Pro Tyr Gly Glu Ser His Leu Phe Arg Val Pro Ser

995

1000

1005

Tyr Gln Ala Leu Leu Arg Gly Val Phe His Gln Thr Val Ser Arg

10

1010

1015

1020

Lys Val Ala Leu Gly

1025

15 <210> 110

<211> 338

<212> PRT

<213> Homo sapiens

<220>

20 <221> Lumican precursor

<222> (1)..(338)

<223> Accession No. as of 29 August 2003: P51884

<400> 110

334/335

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
1 5 10 15
Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln
20 25 30
5 Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro
35 40 45
Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val
50 55 60
Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His
10 65 70 75 80
Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile
85 90 95
Leu Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe
100 105 110
15 Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu
115 120 125
Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu
130 135 140
Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn
20 145 150 155 160
Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val
165 170 175
Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser
180 185 190

335/335

Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu
195 200 205
Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr
210 215 220
5 Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu
225 230 235 240
Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu
245 250 255
Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val
10 260 265 270
Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys
275 280 285
Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser
290 295 300
15 Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser
305 310 315 320
Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr
325 330 335
Leu Asn

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